

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:52:10 ; Search time 46 Seconds  
(without alignments)  
1803.018 Million cell updates/sec

Title: US-10-731-642A-1  
Perfect score: 4534  
Sequence: 1 MFLEKIVDAITGKDDGKKVK.....LFPTSEGGLTGKIPNSVSI 862

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4534	100.0	862	2 S57964	lipoxxygenase (EC 1
2	3934	86.8	862	2 T07775	lipoxxygenase (EC 1
3	3632.5	80.1	861	2 S44940	lipoxxygenase (EC 1
4	3625.5	80.0	859	2 T06352	lipoxxygenase (EC 1
5	3624.5	79.9	859	2 T06339	lipoxxygenase (EC 1
6	3202.5	70.6	859	1 JQ2267	lipoxxygenase (EC 1
7	3137.5	69.2	876	2 T07101	lipoxxygenase (EC 1
8	2911	64.2	878	2 S74207	lipoxxygenase (EC 1
9	2901	64.0	857	2 S01864	lipoxxygenase (EC 1
10	2872	63.3	877	2 T10085	lipoxxygenase (EC 1
11	2837	62.6	861	1 S01142	lipoxxygenase (EC 1
12	2789.5	61.5	865	2 T11852	lipoxxygenase (EC 1
13	2777	61.2	858	2 T12142	lipoxxygenase (EC 1
14	2745.5	60.6	865	1 DASYL1	lipoxxygenase (EC 1
15	2731.5	60.2	864	1 S07075	lipoxxygenase (EC 1
16	2713	59.8	862	2 S22153	lipoxxygenase (EC 1
17	2693	59.4	864	2 S13381	lipoxxygenase (EC 1
18	2689	59.3	856	2 T06596	lipoxxygenase (EC 1
19	2686.5	59.3	853	2 T07662	lipoxxygenase (EC 1
20	2685.5	59.2	853	2 T07036	lipoxxygenase (EC 1
21	2680	59.1	862	2 T05941	lipoxxygenase (EC 1
22	2675	59.0	868	2 T06827	lipoxxygenase (EC 1
23	2660.5	58.7	839	2 T06354	lipoxxygenase (EC 1
24	2660	58.7	868	2 S56655	lipoxxygenase (EC 1
25	2656	58.6	839	1 DASYL2	lipoxxygenase (EC 1
26	2653.5	58.5	859	2 T06429	lipoxxygenase (EC 1
27	2631	58.0	876	2 T05943	probable lipoxxygen
28	2624	57.9	866	2 T06454	probable lipoxxygen
29	2584.5	57.0	864	2 T05945	lipoxxygenase (EC 1

30	2563	56.5	865	1 S23454	lipoxxygenase (EC 1
31	2494	55.0	741	2 S18906	lipoxxygenase (EC 1
32	2002.5	44.2	914	2 T07065	probable lipoxxygen
33	2000.5	44.1	599	2 S18612	lipoxxygenase (EC 1
34	1976.5	43.6	908	2 T07409	lipoxxygenase (EC 1
35	1929.5	42.6	926	2 E96749	probable lipoxxygen
36	1853	40.9	899	2 T11578	probable lipoxxygen
37	1814	40.0	896	2 JQ2391	lipoxxygenase (EC 1
38	1812	40.0	899	2 T07062	probable lipoxxygen
39	1772	39.1	917	2 B96699	probable lipoxxygen
40	1767	39.0	896	2 T07408	lipoxxygenase (EC 1
41	1747.5	38.5	923	2 A53054	lipoxxygenase (EC 1
42	1687	37.2	870	2 T47454	lipoxxygenase AtLOX
43	1678	37.0	517	2 T06274	probable lipoxxygen
44	1655	36.5	623	2 T07664	lipoxxygenase (EC 1
45	1654.5	36.5	936	2 T06190	lipoxxygenase (EC 1

ALIGNMENTS

RESULT 1

S57964

lipoxxygenase (EC 1.13.11.12) - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C;Accession: S57964

R;Veronesi, C.; Fournier, J.; Rickauer, M.; Esquerre-Tugaye, M.T.

submitted to the EMBL Data Library, January 1995

A;Description: Nucleotide sequence of an elicitor-induced tobacco lipoxxygenase cDNA.

A;Reference number: S57964

A;Accession: S57964

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-862 <VER>

A;Cross-references: UNIPROT:Q43800; EMBL:X84040; NID:g899343; PIDN:CAA58859.1; PID:g89934

C;Superfamily: lipoxxygenase

C;Keywords: oxidoreductase

Query Match 100.0%; Score 4534; DB 2; Length 862;  
Best Local Similarity 100.0%; Pred. No. 3.1e-296;  
Matches 862; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 421 EAIKTNRLFILNHHDIILMPYLRRINTSTDTKTYASRLLFLQDNGTLKPSAIELSLPHPD 480

Qy 481 GDQFGAVSKVYTPADQGVESIWOLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNR 540

Db 481 GDQFGAVSKVYTPADQGVESIWOLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNR 540

Qy 541 QLSALHPIYKLLHHPHFRETMINALARQILINGGGLELTLVFPKYSMEMSAVVYKDWVF 600

Db 541 QLSALHPIYKLLHHPHFRETMINALARQILINGGGLELTLVFPKYSMEMSAVVYKDWVF 600

Qy 601 PEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSD 660

Db 601 PEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSD 660

Qy 661 DAVQKOTELQAWWKELREEGHGDKKDEPWPKMQTVQELIDSCITTIWIASALHAAVNF 720

Db 661 DAVQKOTELQAWWKELREEGHGDKKDEPWPKMQTVQELIDSCITTIWIASALHAAVNF 720

Qy 721 QYPYAGYLPNRPRTLNRNFMPEPGSPYEELKTNPDKVFLKTTITPQLQTLGSLIEILSR 780

Db 721 QYPYAGYLPNRPRTLNRNFMPEPGSPYEELKTNPDKVFLKTTITPQLQTLGSLIEILSR 780

Qy 781 HSSDTLYLGQRESPEWTKDQEPPLSAFARFGKKLSIEDQIMQMNVDKWKNSRGPVKVPY 840

Db 781 HSSDTLYLGQRESPEWTKDQEPPLSAFARFGKKLSIEDQIMQMNVDKWKNSRGPVKVPY 840

Qy 841 TLLFPTSEGLTGKIPNSVSI 862

Db 841 TLLFPTSEGLTGKIPNSVSI 862

RESULT 2

T07775

lipoxigenase (EC 1.13.11.12) LX-3 - potato

C:Species: Solanum tuberosum (potato)

C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004

C:Accession: T07775

R:Kolomiets, M.V.; Hannapel, D.J.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z16124

A:Accession: T07775

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-862 <KOL>

A:Cross-references: UNIPROT:Q43191; EMBL:U60202; NID:gl407704; PIDN:AAB67865.1; PID:gl40

A:Experimental source: cv. Berolina

C:Genetics:

A:Gene: LX-3

C:Function:

A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis per

C:Superfamily: lipoxigenase

C:Keywords: fatty acid oxidation; oxidoreductase

Query Match 86.8%; Score 3934; DB 2; Length 862;

Best Local Similarity 85.1%; Pred. No. 6.1e-256;

Matches 735; Conservative 64; Mismatches 61; Indels 4; Gaps 3;

Qy 1 MFLEKIVDAITGK--DDGKKVKGTIVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLELIS 58

Db 1 MLEKIVEAISGRSEDNGKKVGTIVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLELIS 60

Qy 59 SVNADPANGLOQKRKAAYLENWLNSTPIAAGESAFRVTFTDWDDEEFGVPGAFIKNLH 118

Db 61 VHADPGNSLOQKRSPAYLEKWLTTGTSLVAGESAFDVTFDW-DEDIGVPGAFIINNHF 119

Qy 119 FSEFFLKSLTLEDPVNHGKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYRE 178

Db 120 FNEFYLKSLTLEDPVNHGKVHFCVNSWVYPANKYKSERIFFANQAYLPGETPEPLRNYRE 179

Qy 179 NELVTLRGDGTGKLEEDRVYDYAYYNDLGDQDLKQDLSRPLVGGSEYFYPRRGRTRK 238

Db 180 KELVNLGRNGKLEEDRVYDYALYNDLGDPEKQYARTILGGSABEYYPRRGRTRK 239

Qy 239 PTKTDPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLLPEFKALFDSTH 298

Db 240 PTKADPKSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFALKSIVQFLIPEFOALFDSTP 299

Qy 299 NEFDSFEDVLKLYEGGIKLPQGPLLKAITDSIPLEILKELLRSDDGEGLFKYPTPQVIOED 358

Db 300 DEFDSFEDVLKLYEGGIKLPQGPLKALTDSDIPLEILKEIRTDGEGKFKFTPTPQVIOED 359

Qy 359 KTAWRTDDEFGREMLAGVNPVVISRLQEPFPPKSKLDPKIYGNQNSTITREQIEDKLDGLT 418

Db 360 KSSWRTDDEFAREMLAGVNPVVISRLQEPFPPKSQLDSEVYGNQNSTITKEHIENTLDGLT 419

Qy 419 IDEAIKTNRLFILNHHDIILMPYLRRINTSTDTKTYASRLLFLQDNGTLKPSAIELSLPH 478

Db 420 IDDAIKTNRLYILNHHDIILMPYVRRINT-TNTKLYASRLLFLQDDGTMKPVAIELSPLH 478

Qy 479 PDGQDFGAVSKVYTPADQGVESIWOLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIAT 538

Db 479 PDGDELGAVSKVYTPADQGVESIWOLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIAT 538

Qy 539 NRQLSALHPIYKLLHHPHFRETMINALARQILINGGGLELTLVFPKYSMEMSAVVYKDW 598

Db 539 NRQLSVLHPIHKLLHHPHFRTMINALARQILINAGGVLEMTVFPKAYAMEMSAVVYKSW 598

Qy 599 VFPEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYK 658

Db 599 VFPEQALPADLIKRGVAVEDSSSPHGVRLLIQDYPYAVDGLKIWSAISKSWVTEYCNFYK 658

Qy 659 SDDAVQKOTELQAWWKELREEGHGDKKDEPWPKMQTVQELIDSCITTIWIASALHAAVN 718

Db 659 SDELVLKDNELQAWWKELREEGHGDKKDEPWPKMQTROELKDSCTIIWIASALHAAVN 718

Qy 719 FGQYPYAGYLPNRPRTLNRNFMPEPGSPYEELKTNPDKVFLKTTITPQLQTLGSLIEIL 778

Db 719 FGQYPYAGYLPNRPTLRRFMPEPGTPEYEELKTNPDKAYLKTITPQLQTLGSLIEIL 778

Qy 779 SRHSSDTLYLGQRESPEWTKDQEPPLSAFARFGKKLSIEDQIMQMNVDKWKNSRGPVKV 838

Db 779 SRHASDEIYLGQDSSSEWTKDQEPPIAAFERFGKKLSEIEDQIIQMGDKKWKNSRGPVNV 838

Qy 839 PYTLLFPTSEGLTGKIPNSVSI 862

Db 839 PYTLLFPTSEGLTGKIPNSVSI 862

RESULT 3

S44940

lipoxigenase (EC 1.13.11.12) - potato

C:Species: Solanum tuberosum (potato)

C>Date: 06-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C:Accession: S44940

R:Casey, R.

submitted to the EMBL Data Library, May 1994

A:Reference number: S44940

A:Accession: S44940

A:Molecule type: mRNA

A:Residues: 1-861 <CAS>

A:Cross-references: UNIPROT:P37831; EMBL:X79107; NID:g486618; PIDN:CAA55724.1; PID:g48661

C:Superfamily: lipoxigenase

C:Keywords: oxidoreductase

Query Match

80.1%; Score 3632.5; DB 2; Length 861;

Best Local Similarity 78.9%; Pred. No. 1.1e-235;

Matches 672; Conservative 83; Mismatches 94; Indels 3; Gaps 3;

Qy 12 GKDDGKKVKGTVVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLELISSVNADPANGLOQK 71

Db 12 GHDDSKKVKGTVMVMKNVLDFTDLAGSLTGKIFDVLGQKVSFQLISSVQGDPTNGLQK 71

Qy 72 RSKAYLENWLNSTPIAAG-ESAFRVTFTDWDDEEFGVPGAFIKNLHSEFFLKSLTLE 130

Db 72 HSNPAYLENSLFTLTPLTAGSETAFGVTFDW-NEEFGVPGAFIKNMHINEFFLKSLTLE 130

QY	131	DVPNHGKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELVTLRGDGTG	190
Db	131	DVPNHGKVHFCVNSWVYPSLNYKSDRIFFANQYLPSETPELLRKYRENELLTLRGDGTG	190
QY	191	KLEEDRVYDYAYYNDLGDGPKQDLSRPVLGSGSEYYPYPRRGRTGRKPTKTDPNSESRI	250
Db	191	KREAWDRIYDYNDLGNPDQGENVRTTLGGSAAEYYPYPRRGRTGRPTRTDPKSESRI	250
QY	251	PLLMSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLLPEFKALFDSHNEFDSFEDVLKL	310
Db	251	PLILSLDIYVPRDERFGHLKMSDFLTALYSIVQFILPELHALFDGTFNEFDSFEDVLR	310
QY	311	YEGGIKLPQGPLLKAITDSIPLEILKELRSDGEGFLFKYPTPQVIOEDKTAWRTDEEFG	370
Db	311	YEGGIKLPQGPLFKALTAAIPLEMIRELLRTDGEILRFPTPLVIKDSKTAWRTDEEFAR	370
QY	371	EMLAGVNPVIISRLQEPFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIAKTNRLF	430
Db	371	EMLAGVNPVIISRLQEPFPPKSKLDPEAYGNQNSTITAETHIEDKLDGLTIDEAMNNKLF	430
QY	431	LNHHDILMPYLRRINTSTDTKTYASRTLFLQDNGTLKPSAIELSLPHDPDQFGAVSKV	490
Db	431	LNHHDVIIPLYLRINT-TITKAYASRTLFLQDNGSLKPLAIELSFPHDPDQFGVTSKV	489
QY	491	YTPADQGVESGIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQLSALHPIYK	550
Db	490	YTPSDQGVESSIWQLAKAYAVNDVGHQLISHWLNTHAVIEPFVIATNRQLSVLHPIHK	549
QY	551	LLHHPHFRETWNINALARQILINGGGLLELTVPFPAKYSMEMSAVVYKDWVPEQALPTDL	610
Db	550	LLYPHFRDTMNINASARQLLVNAGGVLESTVFQSKFAMEMSAVVYKDWVFPDQALPADLV	609
QY	611	KRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKSDDAVQKOTELQ	670
Db	610	KRGVAVEDSSSPHGVRLIEDYPYAVDGLIWSAIKSWVTDYCSFYGSDDEILKONELQ	669
QY	671	AWWKELREEGHDKKDEPWPMPKMTVQELIDSCITITIIWIASALHAAVFGQYPYAGYLPN	730
Db	670	AWWKELREVGHGDKKNEPWPPEMETPQELIDSCITIIWIASALHAAVFGQYPYAGYLPN	729
QY	731	RPTLSRNFMPPEGSPYEELKTNPKVFLKTTIPQLQTLGLISLIEILSRHSSDTLYLGQ	790
Db	730	RPTVSRRFMPPEPGTPEYEELKRNPKAFKLTITAQLQTLGLVSLVEILSRHTTDEIYLGQ	789
QY	791	RESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPVKVPYTLFLPTSEGG	850
Db	790	RESPEWTKDKEPLAADFDFGKKLTIDIEKQIIQRNGDNILNRSRGPVNAPYTLFLPTSEGG	849
QY	851	LTGKGIPNSVSI 862	
Db	850	LTGKGIPNSVSI 861	
RESULT 4			
T06352			
lipoxxygenase (EC 1.13.11.12) - tomato			
C:Species: Lycopersicon esculentum (tomato)			
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004			
C:Accession: T06352			
R:Kausch, K.D.; Handa, A.K.			
Plant Physiol. 107, 669-670, 1995			
A:Title: Molecular cloning and nucleotide sequence of a lipoxxygenase cDNA from ripening			
A:Reference number: Z15617; MUID:95241637; PMID:7724686			
A:Accession: T06352			
A>Status: preliminary; translated from GB/EMBL/DBBJ			
A:Molecule type: mRNA			
A:Residues: 1-859 <KAU>			
A:Cross-references: UNIPROT:Q42873; EMBL:U13681; NID:G534845; PIDN:AAA74393.1; PID:G5348			
A:Experimental source: Strain Rutgers; tissue-type fruit pericarp			
C:Genetics:			
A:Gene: LOX			
C:Superfamily: lipoxxygenase			
C:Keywords: oxidoreductase			

Query Match		80.0%;	Score 3625.5;	DB 2;	Length 859;
Best Local Similarity		79.4%;	Pred. No. 3.2e-235;		
Matches 685;		Conservative 70;	Mismatches 103;	Indels 5;	Gaps 3;
QY	1	MFLEKIVDAITGKDDGKKVGTVLMKKNVLDFTDINASVLDGVLEFGRRVSLELIS-S	59		
Db	1	MSLGGIVDAILGKDDRPKVGRVILMKKNVLDFINIGASVVDGISDLGQKVSQILISGS	60		
QY	60	VNADPANGLOQKRSKAAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHF	119		
Db	61	VNYD--GLEGKLSNPAYLESWLTDTITAGESTFSVTFDWRDDEFVPGAFIKNLHL	117		
QY	120	SEFFLKSLTLEDVPHGKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYREN	179		
Db	118	NEFFLKSLTLEDVPNYKIHFCVNSWVYPAFRYKSDRIFFANQAYLPSETPQPLRKYREN	177		
QY	180	ELVTLRGDGTGKLEEDRVYDYAYVNDLGDGPKQDLSRPVLGSGSEYYPYPRRGRTGRKP	239		
Db	178	ELVALRGDGTGKLEEDRVYDYACYNLGEPEDKGEYARPILGSGSEYYPYPRRGRTGREGP	237		
QY	240	TKTDPNSESRIPLIMSLDIYVPRDERFGHIKLSDFLTALKSIVQLLLPEFKALFDSH	299		
Db	238	TKADPNCESRNPLPMSLDIYVPRDERFGHVKKSDFLTSSKSSLTQLLLPAFKALCDNTPN	297		
QY	300	EFDSFEDVLKYEGGIKLPQGPLLKAITDSIPLEILKELRSDGEGFLFKYPTPQVIOEDK	359		
Db	298	EFNSFADVLNLYEGGIKLPQEPWLKAITDNISSEILKOILQTDGGLLKYPPTPQVIOGDK	357		
QY	360	TAWRTDEEFGREMLAGVNPVIISRLQEPFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTI	419		
Db	358	TAWRTDEEFGREMLAGSNPVLISRLQEPFPPKSKLDPITYGNQNSTITTEHVQDKLGLTV	417		
QY	420	DEAIKTNRLFILNHHDILMPYLRRINTSTDTKTYASRTLFLQDNGTLKPSAIELSLPH	479		
Db	418	NEAIAKSNRLFILNHHDIVMPLLRKINMSANTKAYASRTLFLQDRTLKPLAIELSLPH	477		
QY	480	DGDFGAVSKVYTPADQGVESGIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATN	539		
Db	478	DGDFGTVSKVYTPADQGVESGIWQFAKAYAVNDMGIHQLISHWLNTHAVIEPFVIATN	537		
QY	540	ROLSALHPIYKLLHHPHFRETWNINALARQILINGGGLLELTVPFPAKYSMEMSAVVYKDW	599		
Db	538	RHLSVLHPIHKLLHHPHFRTNINALARETLTVDGG-FETSLFPAKYSMEMSAAAAAYKOW	596		
QY	600	FPEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKS	659		
Db	597	FPEQALPADLLKRGVAVEDLSSPHGIRLLILDYPYAVDGLIWAIAIKSWVTEYCKFYKS	656		
QY	660	DDAVQKDTLQAWWKELREEGHDKKDEPWPMPKMTVQELIDSCITITIIWIASALHAAVNF	719		
Db	657	DETVEKDTLQAWWKELREEGHDKKDEAWWPKLTQROELRDCCTIIIIWIASALHAAALHF	716		
QY	720	GQPYAGYLPNRPRTLNRNFMPEGSPYEELKTNPKVFLKTTIPQLQTLGLISLIEILS	779		
Db	717	GLYSYAGYLPNRPRTLSCNLMPEGSPYEELKTNPKVFLKTFVPLQSLLEISIFEVSS	776		
QY	780	RHSSDTLYLGQRESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPVKVP	839		
Db	777	RHASDEVYLGQRDSIEWTKDKEPLVAFERFGKMLSDIENRIMMNSHKSWKNRSGPVNVP	836		
QY	840	YTLFPPTSEGLTGKIPNSVSI 862			
Db	837	YTLFPPTSEGLTGKIPNSVSI 859			

RESULT 5

T06339  
lipoxxygenase (EC 1.13.11.12) loxB - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T06339  
R:Perrie, B.J.; Beaudoin, N.; Burkhart, W.; Bowsher, C.G.; Rothstein, S.J.









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Db 264 YESRLSPIMSLDIYVPKDENFGHLKMSDFLGYTLKALSTSIKPLQSI FDVTPNEFDNFK 323
Qy 306 DVLKLYEGGIKLPQGPLLKAITDSIPLEILKELLRSDDGEGLFKYPTPQVIOEDKTAWRD 365
Db 324 EVDNLFERGFPIPN-AFKTLTDLTPPLFKALVRNDGKFLKFPPTPEVVKONKIGWSTD 382
Qy 366 EEFGRMLAGVNPVVISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKT 425
Db 383 EEFAREMLAGPNPLIRRLEAFPPTSCLDPNVYGNQNSTITTEHIIKHGLDGLTVDEAMKQ 442
Qy 426 NRLFILNHHDIIMPYLRRINTSTTKTYASRTLFLQDNGTLKPSAIELSLPHPDGDFG 485
Db 443 NRLYIVDFHDALMPYLTRMN-ATSTKYATRTLILLKDDGTLKPLVIELALPHPDGDLG 501
Qy 486 AVSKVYTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQLSAL 545
Db 502 AISKLYFPAENGVOKSIWQLAKAYTVNDVGYHQLISHWLNTHAVLEPFVIATHRQLSVL 561
Qy 546 HPIYKLLHPHFRETMINALARQILINGGGLLELTVFPKYSMEMSAVVYKDWVPPEQAL 605
Db 562 HPIHKLLVPHYKDTMFINASARQVLINANGLIETTHYPISKYSMELSSILYKDWTFPDQAL 621
Qy 606 PTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSDDAVQK 665
Db 622 PNNLMKRGLAVEDSSAPHGLRLINDYPFAVDGLDIWSAIKTWQDYCCLYYKODNAVQN 681
Qy 666 DTELQAWKELREEGHGDKKDEPWPKMQTVQELIDSCITITWIASALHAAVNFQYPPYA 725
Db 682 DFELQSWNELREKHADKKHEPWPKMQTSLIESCTTIWIASALHAAVNFQYPPYG 741
Qy 726 GYLPNRTLSRNFMPPEPGSPPEYEELKTNPDKVFLKTIPTPOLQTLGLGISLIEILSRHSDT 785
Db 742 GYILNRTTSRRFMPEVGTAEYKELESNPEKAPLRTICSELQALVSIIEILSKHASDE 801
Qy 786 LYLQRESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPVKVPYTLLEP 845
Db 802 VYLGQRASIDWTSDKIALEAFKFGKNLFEVENRIMERKEVNLKNRSGPVNLPYTLVLP 861
Qy 846 TSEGGLTGKGPNSVSI 862
Db 862 SSNEGLTGRGIPNSISI 878

RESULT 9
S01864
lipoxxygenase (EC 1.13.11.12) 3 - soybean
C:Species: Glycine max (soybean)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 28-Apr-1993
C:Accession: S01864
R:Yenofsky, R.L.; Fine, M.; Liu, C.
Mol. Gen. Genet. 211, 215-222, 1988
A:Title: Isolation and characterization of a soybean (Glycine max) lipoxxygenase-3 gene.
A:Reference number: S01864
A:Accession: S01864
A:Molecule type: mRNA
A:Residues: 1-857 <YEN>
A:Cross-references: EMBL:X06928
C:Genetics:
A:Gene: lox-3
A:Introns: 70/1; 165/3; 246/1; 353/1; 381/3; 417/3; 519/2; 607/2
C:Superfamily: lipoxxygenase
C:Keywords: oxidoreductase

Query Match
Best Local Similarity 64.0%; Score 2901; DB 2; Length 857;
Matches 550; Conservative 119; Mismatches 161; Indels 36; Gaps 9;

Qy 16 GKVKGTGVLMKKNVLDFT-----DINASVLDGVLEFLGRRVSLLELISSVNA 62
Db 9 GHKIKGTVLMRKNVLDVNSVTSVGIIQGGLDVGSTDLTLTAFLGRPVSLQISATKA 68
Qy 63 DPANGLQKRSKAAYLENWLNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHFSEF 122
```

```
Db 69 D-ANG-KGKLGKATFLEGIITSLPTLGAGQSAFKINFEWDDGS-GILGAFYIKNFMQTEF 125
Qy 123 FLKSLTLEDVPHGKVHFVNCNSWVYPANKYKSDRIFFANQAYLPSETPDTLTKYRENELV 182
Db 126 FLVSLTLEDIPNHGSIHFVNCNSWIYNAKLFKSDRIFFANQTYLPSETPAPLVKYREEELH 185
Qy 183 TLRGDGTGKLEEDRVVDYAYYNDLGDPPDKQDLSRPVLGSGSSEYPYPRRGRTRGKPKTK 242
Db 186 NLRGDGTGERKEWERYVDYVNDLGDPPDKGENHARVPVLGGNDTFPYPRRGRTRGKPKTRK 245
Qy 243 DPNSERIPLLMSLDIYVPRDEREFGHIKLSDFLTFALKSIVQLLLPEFKALFD--STHNE 300
Db 246 DPNSER-----SNDVYLPDEAFGLKSSDFLTGYLKSVSQNVLPLLQSAFDLNFPTPRE 300
Qy 301 FDSFEDVLKLYEGGIKLPQGPLLKAITDSI-----PLEILKELLRSDDGEGLFKYPTPQVIO 356
Db 301 FDSFDEVHGLYSGGIKLP-----TDIISKISPLPVLKEIFRTDGEQALKFPPPKVIO 352
Qy 357 EDKTAWRTDEEFGREMLAGVNPVVISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDG 416
Db 353 VKSAMWTDDEFAREMLAGVNPNLIRCLKEFPPRSKLDQSVYGDHTSQITKEHLEPNLEG 412
Qy 417 LTIDEAICTNRLFILNHHDIIMPYLRRINTSTDTKTYSARTLLFLQDNGTLKPSAIELSL 476
Db 413 LTVEAIONKRLFLGLGHDPIMPYLRRIN-ATSTKAYATRTILFLKNDGTTLRPLAIELSL 471
Qy 477 PHPDGQFGAVSKVYTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVI 536
Db 472 PHPDGQSGAFSQVFLPADGVESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFII 531
Qy 537 ATNRQLSALHPIYKLLHPHFRETMINALARQILINGGGLLELTVFPKYSMEMSAVVYK 596
Db 532 ATNRHLSVVHPIYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTFLWGRYSVEMSAVVYK 591
Qy 597 DWVFEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYY 656
Db 592 DWVFTDQALPADLIRKGMALIEDPSCPHGIRLVIEDYPYAVDGLIEIWDAIKTWVHEYVFLY 651
Qy 657 YKSDDAVQKDTLQAWKELREEGHGDKKDEPWPKMQTVQELIDSCITITWIASALHAA 716
Db 652 YKSDDTLREDPELQACWKELVEVGHGDKKNEPWWPKMQTREELVEACAIITWTASALHAA 711
Qy 717 VNFQYYPYAGYLPNRPRTLNRNMPPEPGSPPEYEELKTNPKVFLKTIPTPOLQTLGLISLIE 776
Db 712 VNFQYYPYGGIILNRPRTLNRNMPPEKGSAAEYEELRKNPKQAYLKTITPKFQTLIDLVSIE 771
Qy 777 ILSRHSSDTLYLGQRESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPV 836
Db 772 ILSRHASDEVYLGERNPNWTSDFRALEAFKRFGNKLAQIENKLSERNNDEKLNRNCGPV 831
Qy 837 KVPYTLFFPTSEGLTGKGPNSVSI 862
Db 832 QMPYTLLLPSSKEGLTFRGIPNSISI 857
```

RESULT 10

Tl0085  
lipoxxygenase (EC 1.13.11.12) - cucumber  
C:Species: Cucumis sativus (cucumber)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: Tl0085  
R:Matsui, K.; Nishioka, M.; Kajiwara, T.; Hase, T.  
submitted to the EMBL Data Library, September 1995  
A:Reference number: Z16939  
A:Accession: Tl0085  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-877 <MAT>  
A:Cross-references: UNIPROT:Q42705; EMBL:U36339; NID:g1017771; PID:g1017772  
A:Experimental source: cv. Suoyo; tissue type root  
C:Function:  
A:Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis pent  
C:Superfamily: lipoxxygenase







Db 412 FSTLDEAIQNKLFLEHHDHTIIPYLRLLN-STSTKAYASRTILFLKSDGTLKPLAIELS 470  
QY 476 LPHPDGQDFGAVSKVYTPADQGVGSIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFV 535  
Db 471 LPHPGDQDFGVSVNVYLPALIEGVEATIWLLAKAYIVVNDSCFHLQVSHWLHTHAVVEPFV 530  
QY 536 IATNRQLSALHPIYKLLHPHFRETMINALARQILINGGGLLELTVFPKAYSMEMSAVVY 595  
Db 531 IATNRQLSVLHPIYKLLHPHYRDTMINALARQSLVNADGIIIEKFLWGGYAMEISSKVY 590  
QY 596 KDWVFEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNV 655  
Db 591 KDWVFTDQALPADLIKRGIAVEDSTSPHGLRLVIEDYPYAVDGLDIWDAIKTWVQDYVSI 650  
QY 656 YKSDDAVQKDTLQAWKELREEGHGDKKDEPWPWKMTVQELIDSCITITIWIASALHA 715  
Db 651 YYITDDKIQDSELQSWKVEVVEVGHGDKKGPWPKLQTRQDLIHVSSIIWSASALHA 710  
QY 716 AVFNGQYPYAGYLPNRPTLSRNFMPSPGSPYEELKTNPKVFLKTIPTQLTLGISLI 775  
Db 711 AVFNGQYPYGGFILNRPTLSRRLMPEKGTTEYDELATNPQKAYLKTIPTKLQTLIDLSVI 770  
QY 776 EILSRHSSDTLYLGQRESPE-WTKDQEPISAFARFGKCLSDIEDQIMQMVNDEKWNRS 834  
Db 771 EILSRHASDEYYLGORDSAEYWTSDTNALAAFKKFGKTLAEIEGQLILRNNNESLNRVG 830  
QY 835 PVKVPYTLFPPTSEGGTLTKGIPNSVSI 862  
Db 831 PVSMPTLLYPSSEGLTFRGIPNSISI 858

RESULT 14

DASYL1  
lipoxxygenase (EC 1.13.11.12) 2 - soybean  
N;Alternate names: carotene oxidase 2; lipoxidase 2  
C;Species: Glycine max (soybean)  
C;Date: 31-Mar-1989 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
C;Accession: A28161; A30831; A37160; S13536  
R;Shibata, D.; Steczko, J.; Dixon, J.E.; Andrews, P.C.; Hermodson, M.; Axelrod, B.  
J. Biol. Chem. 263, 6816-6821, 1988  
A;Title: Primary structure of soybean lipoxxygenase L-2.  
A;Reference number: A28161; MUID:88198254; PMID:2834391  
A;Accession: A28161  
A;Molecule type: mRNA  
A;Residues: 1-865 <SH1>  
A;Cross-references: UNIPROT:P09439; GB:J03211; NID:g170013; PIDN:AAA33987.1; PID:g170014  
A;Note: there are no disulfide bonds  
R;Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.  
Plant Mol. Biol. 7, 11-23, 1986  
A;Title: Two soybean seed lipoxxygenase nulls accumulate reduced levels of lipoxxygenase b  
A;Reference number: A30831  
A;Accession: A30831  
A;Molecule type: mRNA  
A;Residues: 232-262,'NL',265-312,'Y',314-362,'E',364-399,'P',401-427,'H',429-485,'G',487  
A;Cross-references: GB:M16876  
A;Experimental source: clone pLX-65  
A;Note: due to a frameshift error, residues in the region 691-865 do not correspond to t  
A;Note: this sequence has been revised in reference A37160  
R;Start, W.G.; Ma, Y.; Polacco, J.C.; Hildebrand, D.F.; Freyer, G.A.; Altschuler, M.  
unpublished results, cited by Yenofsky, R.L., Fine, M., and Liu, C., in Mol. Gen. Genet.  
A;Reference number: A37160  
A;Accession: A37160  
A;Molecule type: mRNA  
A;Residues: 232-262,'NL',265-312,'Y',314-399,'PK',402-427,'H',429-485,'G',487-501,'G',50  
A;Note: this is a revision to the sequence from reference A30831  
R;Shibata, D.; Kato, T.; Tanaka, K.  
Plant Mol. Biol. 16, 353-359, 1991  
A;Title: Nucleotide sequences of a soybean lipoxxygenase gene and the short intergenic re  
A;Reference number: S13381; MUID:91370880; PMID:1909908  
A;Accession: S13536  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 859-865 <SH2>  
A;Cross-references: EMBL:X56139; NID:g18745; PIDN:CAA39605.1; PID:g829267  
C;Comment: In soybean, four isozymes are found with distinct electrophoretic properties.  
C;Function:  
A;Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis pent  
C;Superfamily: lipoxxygenase  
C;Keywords: fatty acid oxidation; iron; metalloprotein; oxidoreductase  
C;Keywords: iron (His, His, Asn, Ile) #status predicted  
F;527,532,718,722,865/Binding site: iron (His, His, Asn, Ile) #status predicted

Query Match 60.6%; Score 2745.5; DB 1; Length 865;  
Best Local Similarity 59.6%; Pred. No. 4.le-176;  
Matches 526; Conservative 129; Mismatches 190; Indels 37; Gaps 11;

QY 1 MFLEKIVDAITGDKDKVKVGTVVLMKKNVLD-----TDIN--ASVLD 42  
Db 1 MFSVPGVSGILNRGGGHKIKGTIVLMRKNVLDNFNSVADLTCKGNVGLIGTLNVVGSTLD 60  
QY 43 GVLEFLGRRVSLELISSVNADPANGLOGKRSKAAYLENWLNTSTPIAAGESAFRVTFDWD 102  
Db 61 NLTAFLGRSVALQLISATK-PLANG-KGKVGKDTFLEGIIIVSLPTLGAGESAFNIQFEW- 117  
QY 103 DEEFGVPGAFIINKLHFSEFFLKSLTLEDVPHGKGVHVCNWSVYPANKYKSDRIFFANQ 162  
Db 118 DESMGIPGAFYIKNYMQVEFYLKSLTLEDVPNQGTIRFVCNWSVYNTKLYKSVRIFFANH 177  
QY 163 AYLPSETPDLRKYRENELVTLRGDGTGKLEEDRVDYDAYYNDLGDPPDKQDLSRPVLG 222  
Db 178 TYVSETPAALVGYREEELKNLRGDKGERKEHDRIYDYVYNDLGNPDHGFARPILG 237  
QY 223 GSSEYPPRRGRTGRKPTKTDPNSSESRIPLLSLDIYVPRDERFGHIKLSDFLTALKSI 282  
Db 238 GSSTHPYPRGRTGRYPTRKDQNSEK-----PGEVYVPRDENFGHLKSSDFLAYGIKSL 291  
QY 283 VQLLLPEFKALFD--STHNEPDSFEDVLKLYEGGIKLPQGFLKAITDSIPLEILKELLR 340  
Db 292 SQYVLPAPAFESVFDLNTFTPNEDSFQDVRDLHEGGIKLP----TEVISTIMPLPVVKELFR 347  
QY 341 SDGEGLFKYPTPQVIOEDKTAWRTDEEFGREMLAGVNPVVISRLQEPFPKSKLDPKIYGN 400  
Db 348 TDGEOVLKFPFPHVIVQVSKSAWMTDEEFAREMVAGVNPVCVIRGLQEPFPKSNLDPITYGE 407  
QY 401 QNSTITREQIEDKLDGLTIDEAKTNRLFLILNHHDILMPYLRINTSTDTKTYASRTLLF 460  
Db 408 QTSKITADALD--LDGYTVDEALASRRLFMLDYHDVFMPIYRRIN-QTYAKAYATRTILF 464  
QY 461 LODNGTLKPSAIELSLPHPDGQFGAVSKVYTPADQGVGSIWQLAKAYAAVNDSGVHQL 520  
Db 465 LRENGTLKPAVIELSLPHPAGLSGAVSQVILPAKEGVESTIWLAKAYVVVNDSCYHQL 524  
QY 521 ISHWLNTAAIEPFVIATNRQLSALHPIYKLLHPHFRETMINALARQILINGGGLLELT 580  
Db 525 MSHWLNTHAVIEPFIIATNRHLSALHPIYKLLTTPHYRDTMINALARQSLINADGIIIEKS 584  
QY 581 VEPKYSMEMSAVVYKDWVFEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLK 640  
Db 585 FLPSKHSEMEMSSAVYKNWVFTDQALPADLIKRGVAIKDPSAPHGLRLLLIEDYPYAVDGLE 644  
QY 641 IWSAISKWVTEYCNYYKSDDAVQKDTLQAWKELREEGHGDKKDEPWPWKMTVQELI 700  
Db 645 IWSAIAKTWVQEVSLYARDDVVKPDSELOQWKEAVEKRGHGDLDKDPWPKLQTIIELV 704  
QY 701 DSTITIWIASALHAAVNFQYYPYAGYLPNRPTLSRNFMPSPGSPYEELKTNPDKVFLK 760  
Db 705 EICTIIWTASALHAAVNFQYYPYGGFILNRPTSSRLLPEKGTPEYEEMVKSQKAYLR 764  
QY 761 TITPQLQTLGSLIEILSRHSSDTLYLGQRESPEWTKDQEPISAFARFGKCLSDIEDQI 820  
Db 765 TITSKFQTLVDLSVIEILSRHASDEVYLGQRDNPHWTSDSKALQAFQKFGNKLKEIEEKL 824  
QY 821 MQMNVDEKWNRSRGPVKVYPTLLFPTSETGGTLTKGIPNSVSI 862  
Db 825 ARKNNDQSLNRLGVPQLPYTLHLHPNSE-GLTCRGIPNSISI 865

RESULT 15  
S07075  
lipoxxygenase (EC 1.13.11.12) 2 [similarity] - garden pea  
C;Species: Pisum sativum (garden pea)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: S07075  
R;Ealing, P.M.; Casey, R.  
Biochem. J. 264, 929-932, 1989  
A;Title: The cDNA cloning of a pea (Pisum sativum) seed lipoxxygenase. Sequence comparisc  
A;Reference number: S07075; MUID:90147555; PMID:2515855  
A;Accession: S07075  
A;Molecule type: mRNA  
A;Residues: 1-864 <EAL>  
A;Cross-references: UNIPROT:P14856; EMBL:X17061; NID:g20801; PIDN:CAA34906.1; PID:g20802  
C;Superfamily: lipoxxygenase  
C;Keywords: oxidoreductase

Query Match 60.2%; Score 2731.5; DB 1; Length 864;  
Best Local Similarity 60.1%; Pred. No. 3.6e-175;  
Matches 526; Conservative 129; Mismatches 183; Indels 37; Gaps 11;

Qy	10	ITG-KDDGKKVKGTVVLMKKNVLDFT-----DINASVLGDGVLEFLGR 50
Db	5	VTGLLNKGHKIRGTVLMRKNVLDFTIVSIGGNNVGHVIDSGINIGSTLDGLTAFLGR 64
Qy	51	RVSLELISSVNADPANGLOGKRSKAAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPG 110
Db	65	SVSLQLISATKSD-ANG-KGKVGKDTFLEGVLASPTLGAGESAFNIHFEW-DHEMGIPG 121
Qy	111	AFITIKNLHFSEFFLKSLTLEDVPHGKVFHVCNSWVYPANKYKSDRIFFANQAYLSETP 170
Db	122	AFYIKNYMQVEFFLKSLTLEDVPHNGTIRFVCNSWVYNSKLYKSPRIFFANKSYLPSETP 181
Qy	171	DTLRKYRENELVTLRGDGTGKLEBWRVYDYAYYNDLGDPKGQDLSRPLVSGSSEYPYP 230
Db	182	SPLVKYREEELQTLRGDGTGERKLHERIYDYDVYNDLGNPDGHEHLARPILGGSSTHPYP 241
Qy	231	RRGRTGRKPTKTDPNSESRIPLMSLDIYVPRDERFGHIKLSDFLTFAFKSIVQLLPEF 290
Db	242	RRGRTGRYPTRKDPNSEK-----PATETYVPRDENFGLKSSDFLAYGIKSVSQCVPAF 296
Qy	291	KALFD--STHNEFDSFEDVLKLYEGGIKLPQGPLLKAITDSIPLLEILKELLRSDDGEGLEK 348
Db	297	ESAFDLNFTPNEFDSFDVRNLFEGGIKLP---LDVISLSPLPVVKEIFRTDGEQVLK 352
Qy	349	YPTPQVIQEDKTAWRTDEEFGREMLAGVNPVVISRLQEPFKSKLDPKIYGNQNSTITRE 408
Db	353	FTPPHVIRVSKSAWMTDEEFAREMLAGVNPCMIRGLQEPFKSNLDPAPAEYGDHTSKISVD 412
Qy	409	QIEDKLDGLTIDEAIAKTNRLFILNHHDLMPYLRRINTSTDTKTYASRTLFLQDNGLTK 468
Db	413	VL--NLDGCTIDEALASGRFLFDYHDTFIPFLRRIN-ETSAKAYATRTILFLKENGTLK 469
Qy	469	PSAIELSLPHPDGQDFGAVSKVYTPADQGVGSIWQLAKAYAAVNDSGVHQLISHWLNTH 528
Db	470	PVAIELSLPHPDGDKSGFVKVILPADEGVESTIWLLAKAYVVVNDSCYHQLMSHWLNTH 529
Qy	529	AAIEPFVIATNRQLSALHPIYKLLHHPRET-MNINALARQILINGGGLLELTVPFAKYS 587
Db	530	AVIEPFVIATNRQLSVVHPINKLLAPHYRDTMMNINALARDSLINANGLIERSFLPSKYA 589
Qy	588	MEMSAVYKDWVFPEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAICS 647
Db	590	VEMSSAVYKYVWFTDQALPNDLTIKRNNAVKDSPPYGLRLLIEDYPYAVDGLLEIWTAKT 649
Qy	648	WVTEYCNYYKSDDAVQKDTTELQAWWKELREEGHGDKDEPWWPKMQTVQELIDSCITTI 707
Db	650	WVQDYVSLYATDNDIKNDSELQHWKVEVEKGHGDLKOKPWWPKLQTFDELVEVCTIII 709
Qy	708	WIASALHAAVNFQYYPYAGYLPNRPTLSRNFMPPEPGSPYEELKTNPDKVFLKTTITPQLQ 767
Db	710	WTASALHAAVNFQYYPYGGIILNRPRTLRRLLPEEGTAEYDEMVKSSQKAYLRTITPKFQ 769

Qy	768	TLIGISLIEILSRHSSDTLYLGORESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVD 827
Db	770	TLIDLSVIEILSRHASDEVYLGQRENPHWTSKALQAFQKFGNKLAEIEAKLTNKNNDP 829
Qy	828	KWKNRSGPVKVPYTYLLFPTSEGGLTGKGIPNSVSI 862
Db	830	SLYHRVGPVQLPYTYLLHPSSKEGLTFRGIPNSISI 864

Search completed: March 10, 2005, 19:02:52  
Job time : 50 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:40:16 ; Search time 178 Seconds  
(without alignments)  
2479.844 Million cell updates/sec

Title: US-10-731-642A-1  
Perfect score: 4534  
Sequence: 1 MFLEKIIVDAITGKDDGKVK.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4534	100.0	862	2 Q43800	Q43800 nicotiana t
2	4095	90.3	862	2 Q9FT17	Q9ft17 lycopersico
3	3934	86.8	862	2 Q43191	Q43191 solanum tub
4	3819.5	84.2	861	2 Q6X5R8	Q6x5r8 nicotiana a
5	3816.5	84.2	861	2 Q6X5R7	Q6x5r7 nicotiana a
6	3695	81.5	857	2 Q41238	Q41238 solanum tub
7	3693	81.5	860	2 Q43190	Q43190 solanum tub
8	3688	81.3	860	1 LOXA_LYCES	P38415 lycopersico
9	3643.5	80.4	861	2 Q24379	Q24379 solanum tub
10	3641.5	80.3	861	2 Q9SC16	Q9sc16 solanum tub
11	3634.5	80.2	861	2 Q22508	Q22508 solanum tub
12	3633.5	80.1	864	2 Q49150	Q49150 solanum tub
13	3632.5	80.1	861	1 LOX1_SOLTU	P37831 solanum tub
14	3625.5	80.0	859	2 Q42873	Q42873 lycopersico
15	3625.5	80.0	861	2 Q43189	Q43189 solanum tub
16	3624.5	79.9	859	1 LOXB_LYCES	P38416 lycopersico
17	3622.5	79.9	861	2 Q22507	Q22507 solanum tub
18	3603.5	79.5	844	2 Q9SAP1	Q9sap1 solanum tub
19	3550	78.3	873	2 Q93YI8	Q93yi8 corylus ave
20	3455.5	76.2	862	2 Q9LEA9	Q9lea9 prunus dulc
21	3424.5	75.5	862	2 Q8W4X6	Q8w4x6 prunus dulc
22	3403	75.1	865	2 Q93WZ2	Q93wz2 gossypium h
23	3288.5	72.5	884	2 Q7X9G5	Q7x9g5 fragaria an
24	3228	71.2	857	2 Q8GV02	Q8gv02 brassica na
25	3202.5	70.6	859	1 LOX1_ARATH	Q06327 arabidopsis
26	3137.5	69.2	876	2 Q41430	Q41430 solanum tub
27	3106	68.5	881	2 Q9M463	Q9m463 cucumis sat
28	3066.5	67.6	697	2 Q24377	Q24377 solanum tub
29	3054	67.4	854	2 Q9FNX7	Q9fnx7 arabidopsis
30	3037	67.0	882	2 Q9LUW0	Q9luw0 arabidopsis
31	3003.5	66.2	858	2 Q9ZU05	Q9zu05 persea amer

32	2914	64.3	878	2 Q42704	Q42704 cucumis sat
33	2911	64.2	878	2 Q42710	Q42710 cucumis sat
34	2894	63.8	857	1 LOX3_SOYBN	P09186 glycine max
35	2872	63.3	877	2 Q42705	Q42705 cucumis sat
36	2837	62.6	861	1 LOX3_PEA	P09918 pisum sativ
37	2793.5	61.6	877	2 Q8S6D6	Q8s6d6 oryza sativ
38	2789.5	61.5	865	2 Q24320	Q24320 phaseolus v
39	2782.5	61.4	864	2 Q8W0V2	Q8w0v2 zea mays (m
40	2779.5	61.3	864	2 Q9AXG8	Q9axg8 zea mays (m
41	2777	61.2	858	2 Q04919	Q04919 vicia faba
42	2746	60.6	866	2 Q39870	Q39870 glycine max
43	2745.5	60.6	865	1 LOX2_SOYBN	P09439 glycine max
44	2731.5	60.2	864	1 LOX2_PEA	P14856 pisum sativ
45	2730.5	60.2	866	2 Q8S6D9	Q8s6d9 oryza sativ

ALIGNMENTS

RESULT 1  
Q43800  
ID Q43800 PRELIMINARY; PRT; 862 AA.  
AC Q43800;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Lipoxigenase (EC 1.13.11.12).  
GN Name=Lox1;  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiiids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cell suspension;  
RA Veronesi C., Fournier J., Rickauer M., Marolda M.,  
RA Esquerre-Tugaye M.T.;  
RT "Nucleotide sequence of an elicitor-induced tobacco lipoxigenase cDNA (PGR95-009).";  
RL Plant Physiol. 108:1342-1342(1995).  
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of  
CC diverse aspects of plant physiology including growth and  
CC development, pest resistance, and senescence or responses to  
CC wounding (By similarity).  
CC -!- CATALYTIC ACTIVITY: Linoate + O(2) = (9Z,11E)-(13S)-13-  
CC hydroperoxyoctadeca-9,11-dienoate.  
CC -!- COFACTOR: Iron (By similarity).  
CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
CC -!- SIMILARITY: Contains 1 PLAT domain.  
DR EMBL; X84040; CAA58859.1; -.  
DR PIR; S57964; S57964.  
DR HSSP; P08170; 1FGT.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR GO; GO:0016165; F:lipoxigenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR000907; Lipoxigenase.  
DR InterPro; IPR01024; Lipoxigenase\_LH2.  
DR InterPro; IPR001246; Plant\_lipoxynse.  
DR InterPro; IPR008976; PLAT\_LH2.  
DR Pfam; PF00305; Lipoxigenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PRO0087; LIPOXYGENASE.  
DR PRINTS; PRO0468; PLTLPOXGNASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS0081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS0095; PLAT; 1.  
KW Dioxigenase; Oxidoreductase.  
SQ SEQUENCE 862 AA; 97552 MW; D2E7B8D323D5CE34 CRC64;

Query Match 100.0%; Score 4534; DB 2; Length 862;

Best Local Similarity 100.0%; Pred. No. 1.1e-293;		Matches 862; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MFLEKIVDAITGKDDGKKVGT	VVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLELISSV 60
Db	1	MFLEKIVDAITGKDDGKKVGT	VVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLELISSV 60
Qy	61	NADPANGIQKRSKAAAYLENWLT	NSTPIAAGESAFRVTFDWDDDEFGVPGAFIINKLHFS 120
Db	61	NADPANGIQKRSKAAAYLENWLT	NSTPIAAGESAFRVTFDWDDDEFGVPGAFIINKLHFS 120
Qy	121	EFFLKSLTLEDVPHGKVHFCVNC	SWVPYANKYKSDRIFFANQAYLPSETPTDLRKYRENE 180
Db	121	EFFLKSLTLEDVPHGKVHFCVNC	SWVPYANKYKSDRIFFANQAYLPSETPTDLRKYRENE 180
Qy	181	LVTLRGDTGKLEEDRVVDYAYN	DLGDPDKQDLSRPVLGGSSEYPYPRRGRTGRKPT 240
Db	181	LVTLRGDTGKLEEDRVVDYAYN	DLGDPDKQDLSRPVLGGSSEYPYPRRGRTGRKPT 240
Qy	241	KTDPNSESRIPLMLSLDIYVPR	DERFGHIKLSDFLTFALKSIVQLLLPEFKALFDSTHNE 300
Db	241	KTDPNSESRIPLMLSLDIYVPR	DERFGHIKLSDFLTFALKSIVQLLLPEFKALFDSTHNE 300
Qy	301	FDSFEDVLKLYEGGIKLPQG	PLLKAITDSIPLEILKELRSDEGLFKYPTPQVQIEDKT 360
Db	301	FDSFEDVLKLYEGGIKLPQG	PLLKAITDSIPLEILKELRSDEGLFKYPTPQVQIEDKT 360
Qy	361	AWRTDEFGREMLAGVNPV	IIISRLQEFPPKSLDPKINYGNONSTITREQIEDKLDGLTID 420
Db	361	AWRTDEFGREMLAGVNPV	IIISRLQEFPPKSLDPKINYGNONSTITREQIEDKLDGLTID 420
Qy	421	EAIKTNRLFILNHHDI	LMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPD 480
Db	421	EAIKTNRLFILNHHDI	LMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPD 480
Qy	481	GDQFGAVSKVYTPADQ	GVESIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNR 540
Db	481	GDQFGAVSKVYTPADQ	GVESIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNR 540
Qy	541	QLSALHPIYKLLHPHF	RETMINALARQILINGGELLETFVPPAKYSMEMSAVVYKDWF 600
Db	541	QLSALHPIYKLLHPHF	RETMINALARQILINGGELLETFVPPAKYSMEMSAVVYKDWF 600
Qy	601	PEQALPTDLIKRGVAV	EDSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSD 660
Db	601	PEQALPTDLIKRGVAV	EDSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSD 660
Qy	661	DAVQKDTLQAWWKEL	REEGHGDKDEPWPMPKMTVQELIDSCITITIWIASALHAAVNFG 720
Db	661	DAVQKDTLQAWWKEL	REEGHGDKDEPWPMPKMTVQELIDSCITITIWIASALHAAVNFG 720
Qy	721	QYPYAGYLPNRP	TLRSNFMEPGSPYEELKTNPDKVFLKTTITPQLQTLGSLIEILSR 780
Db	721	QYPYAGYLPNRP	TLRSNFMEPGSPYEELKTNPDKVFLKTTITPQLQTLGSLIEILSR 780
Qy	781	HSSDTLYLGQRESPE	WTKDQEPLSAFARFGKKLSDIEDQIMQMVNDEKWKNRSGPVKVPY 840
Db	781	HSSDTLYLGQRESPE	WTKDQEPLSAFARFGKKLSDIEDQIMQMVNDEKWKNRSGPVKVPY 840
Qy	841	TLLFFTSEGGLTGK	GIPNSVSI 862
Db	841	TLLFFTSEGGLTGK	GIPNSVSI 862

RESULT 2  
Q9FT17  
ID Q9FT17 PRELIMINARY; PRT; 862 AA.  
AC Q9FT17;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Lipoxxygenase (EC 1.13.11.12).  
QS Lycopersicon esculentum (Tomato).

OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC	lamids; Solanales; Solanaceae; Solanum.
OX	NCBI_TaxID=4081;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Leaf;
RA	Pan Z., Feng Q., Gilchrist D.G., Bostock R.M.;
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC	-!- FUNCTION: Plant lipoxxygenase may be involved in a number of
CC	diverse aspects of plant physiology including growth and
CC	development, pest resistance, and senescence or responses to
CC	wounding (By similarity).
CC	-!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC	hydroperoxyoctadeca-9,11-dienoate.
CC	-!- COFACTOR: Iron (By similarity).
CC	-!- SIMILARITY: Belongs to the lipoxxygenase family.
CC	-!- SIMILARITY: Contains 1 PLAT domain.
DR	EMBL; AY008278; AAG21691.1; -.
DR	HSSP; P08170; 1F8N.
DR	GO; GO:0005506; F:iron ion binding; IEA.
DR	GO; GO:0016165; F:lipoxxygenase activity; IEA.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR000907; Lipoxxygenase.
DR	InterPro; IPR001024; Lipoxxygenase LH2.
DR	InterPro; IPR008976; PLAT_LH2.
DR	Pfam; PF00305; Lipoxxygenase; 1.
DR	Pfam; PF01477; PLAT; 1.
DR	PRINTS; PR00087; LIPOXYGENASE.
DR	PRINTS; PR00468; PLTLPOXGNASE.
DR	SMART; SM00308; LH2; 1.
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR	PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR	PROSITE; PS50095; PLAT; 1.
KW	Dioxygenase; Oxidoreductase.
SQ	SEQUENCE 862 AA; 97504 MW; F2E03A209C8B7714 CRC64;

Query Match 90.3%; Score 4095; DB 2; Length 862;  
Best Local Similarity 88.3%; Pred. No. 2.2e-264;  
Matches 762; Conservative 55; Mismatches 44; Indels 2; Gaps 2;

Qy	1	MFLEKIVDAITGKDDGKKVGT	VVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLELISSV 60
Db	1	MILNKIVDSITGKDDGKKVGT	VVLMKKNVLDFTDVTASIVDGALEFLGRRVSFOLISN- 59
Qy	61	NADPANGIQKRSKAAAYLENWLT	NSTPIAAGESAFRVTFDWDDDEFGVPGAFIINKLHFS 120
Db	60	SVHDANGLEGKLSNPAYLENW	ITNITPVVAGESTFSTFDWDDDEFGVPGAFIINKLHFS 119
Qy	121	EFFLKSLTLEDVPHGKVHFCVNC	SWVPYANKYKSDRIFFANQAYLPSETPTDLRKYRENE 180
Db	120	EFFLKSLTLEHVPNHGKVHFCVNC	SWVPYASKYKSDRIFFANQAYLPSETPELLRKYRENE 179
Qy	181	LVTLRGDTGKLEEDRVVDYAYN	DLGDPDKQDLSRPVLGGSSEYPYPRRGRTGRKPT 240
Db	180	LVALRGDTGKLEEDRVVDYAYN	DLGDPDKQGEYARPVLCGSSQYPYPRRGRTGRKPT 239
Qy	241	KTDPNSESRIPLMLSLDIYVPR	DERFGHIKLSDFLTFALKSIVQLLLPEFKALFDSTHNE 300
Db	240	KTDPNTESRIPLMLSLDIYVPR	DERFGHVKMSDFLTFALKSISQLLLPEFKALFDSTPNE 299
Qy	301	FDSFEDVLKLYEGGIKLPQG	PLLKAITDSIPLEILKELRSDEGLFKYPTPQVQIEDKT 360
Db	300	FDSFADVLKIYEGGIKLPQG	PLFKAIVDAIPLEILKQLLSTDGEGLLKYPTPQVQIEDKS 359
Qy	361	AWRTDEFGREMLAGVNPV	IIISRLQEFPPKSLDPKINYGNONSTITREQIEDKLDGLTID 420
Db	360	AWRTDEFGREMLAGINPV	IIISRLQEFPPKSLDPKINYGNQTSITITREQIEDKLDGLTVD 419
Qy	421	EAIKTNRLFILNHHDI	LMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPD 480

Db 420 EAVKTNRLFILNHHDIIMPYVRRINTTTNTKMYATRLLFLQDDGTLKPLAIELSLPHPD 479

QY 481 GDQFGAVSKVYTPADQGVGSIWOLAKAYAAVNDSGVHQLISHWLNTHAIEPFFVIATNR 540

Db 480 GDQFGAVSEVFTPSDQGVGSIWOLAKAYAAVNDSGVHQLVSHWLNTHTVIEPFFVIATNR 539

QY 541 QLSALHPIYKLLHPHRETMINALARQILINGGGLLELTVFPAKYSMEMSAVVYKDWVF 600

Db 540 QLSVLHPHKLHLLPHFRDTMINALARQILINGGGLLELTVFPAKYSMELSSVIYKDWIF 599

QY 601 PEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWTEYCNYYKSD 660

Db 600 PEQALPADLIKRGVAVEDSNSPHGVRLLIQDYPYAVDGLEIWSAIKSWTEYCNYYKSD 659

QY 661 DAVQKDTLQAWKELREEGHGDKKDEPWPMPKMTVQELIDSCITITIWIASALHAAVNF 720

Db 660 DAVQKDAELQAWKELREEGHGDKKDEPWPMPKMQSVQELIDSCITITIWIASALHAAVNF 719

QY 721 QYPYAGYLPNRPTLSRNFMPPEPGSPSEYEELKTNPDKVFLKTTIPQLQTLIGISLIELSR 780

Db 720 QYPYAGYLPNRPTLSRKFMPEPGSAEYEELKRNPDNVFLKTTIPQLQTLIGISLIELLSR 779

QY 781 HSDTTLYGQRESPEWTKDQEPLSAFARFGKLSIEDIQIMQNVNDEKWNRSRGPVKVP 839

Db 780 HASDTTLYGQDPSPEWTKDQEPLSAFERFGKLGIEIDRIIQMNGDNQKWNRSRGPVKVP 839

QY 840 YTLLFPTSEGGLTGKIPNSVSI 862

Db 840 YTLLFPTSEGLTGKIPNSVSI 862

RESULT 3

Q43191

ID Q43191 PRELIMINARY; PRT; 862 AA.

AC Q43191;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Lipoxxygenase (EC 1.13.11.12).

GN Name=POTLX-3;

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4113;

RN [1]

RP SEQUENCE FROM N.A.

RA Kolomiets M.V., Hannapel D.J., Gladon R.J.;

RT "Nucleotide Sequence of a cDNA Clone for a Lipoxxygenase from Abscisc

RT Acid-Treated Potato Leaves (Accession No. U60202) (PGR96-069).";

RL Plant Physiol. 112:446-446(1996).

CC -!- FUNCTION: Plant lipoxxygenase may be involved in a number of

CC diverse aspects of plant physiology including growth and

CC development, pest resistance, and senescence or responses to

CC wounding (By similarity).

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron (By similarity).

CC -!- SIMILARITY: Belongs to the lipoxxygenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

DR EMBL; U60202; AAB67865.1; -.

DR PIR; T07775; T07775.

DR HSSP; P08170; 1FGT.

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0016165; F:lipoxxygenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000907; Lipoxxygenase.

DR InterPro; IPR001024; Lipoxxygenase\_LH2.

DR InterPro; IPR001246; Plant\_lipoxygns.

DR InterPro; IPR008976; PLAT\_LH2.

DR Pfam; PF00305; Lipoxxygenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PR00087; LIPOXYGENASE.

DR PRINTS; PR00468; PLTLPOXGNASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.

DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.

DR PROSITE; PS50095; PLAT; 1.

KW Dioxxygenase; Oxidoreductase.

SQ SEQUENCE 862 AA; 97777 MW; 94667A9F56041E89 CRC64;

Query Match 86.8%; Score 3934; DB 2; Length 862;

Best Local Similarity 85.1%; Pred. NO. 1.2e-253;

Matches 735; Conservative 64; Mismatches 61; Indels 4; Gaps 3;

QY 1 MFLEKIVDAITGK--DDGKKVKGTVMKKNVLDFTDINASVLDGVLEFLGRRVSLLEIS 58

Db 1 MLEKIVEAISGRSEDNGKKVGTIVLMKKNVLDNFNDVNASLLDGVLEFLGKRVSLQLIS 60

QY 59 SVNADPANGLOGKRSKAAYLENLWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLH 118

Db 61 VVHADPGNSLOGKRSNPAYLEKWLTTGTSLVAGESAFDVTFDW-DEDIGVPGAFIINN 119

QY 119 FSEFFLKSLTLEDVPHGKVHFCNSWVYVANKYKSDRIFFANQAYLPSETPDTLRKYRE 178

Db 120 FNEFYKLSLTLEDVPHGNVHFCNSWVYVPAKKYKSERIFFANQAYLPGETPEPLRNYRE 179

QY 179 NELVTLRGDGTGLEEWRVYDYAYYNDLGDGPKQDLSRPVLGGSSEYPYPRRGRTRGRK 238

Db 180 KELVNLRGNGKLEEWRVYDYALYNDLGDGPEKQYARTILGSAEYYPYPRRGRTRGRK 239

QY 239 PTKTDPNSESRIPLLMSLDIYVPRDERFGHIKLSDFLTFAKLSIVQLLPEFKALFDSTH 298

Db 240 PTKADPKSESRIPLLMSLDIYVPRDERFGHIKLSDFLTYALKSIVQFLIPEFQALFDSTP 299

QY 299 NEFDSFEDVLKLYEGGIKLPOGPLLKAITDSIPLEILKELLRSDEGGLFKYPTPQVIQED 358

Db 300 DEFDSFEDVLKLYEGGIKLPOGPLLKAITDSIPLEILKEIIRTDEGKFKFPTPQVIQED 359

QY 359 KTAWRTDEEFGREMLAGVNPVVISRLQEFFPKSKLDPKIYGNQNSTITREQIEDKLDGLT 418

Db 360 KSSWRTDEEFAREMLAGVNPVVISRLQEFFPKSQDSEVYGNQNSTITKEHIENTLDGLT 419

QY 419 IDEAIKTNRLFILNHHDIIMPYRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPH 478

Db 420 IDDAIKTNRLYILNHHDIIMPYVRRINT-TNTKLYASRTLLFLQDDGTMKPVAIELSLPH 478

QY 479 PDGQFGAVSKVYTPADQGVGSIWOLAKAYAAVNDSGVHQLISHWLNTHAIEPFFVIAT 538

Db 479 PDGDELGAVSKVYTPADQGVGSIWOLAKAYAVAVNDSGVHQLISHWLNTHAIEPFFVIAT 538

QY 539 NRQLSALHPIYKLLHPHRETMINALARQILINGGGLLELTVFPAKYSMEMSAVVYKDW 598

Db 539 NRQLSVLHPHKLHLLPHFRDTMINALARQILINAGGVLEMTVFPKAYAMEMSAAVVYKSW 598

QY 599 VFPEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWTEYCNYYK 658

Db 599 VFPEQALPADLIKRGVAVEDSSSPHGVRLLIQDYPYAVDGLKIWSAIKSWTEYCNFYK 658

QY 659 SDDAVQKDTLQAWKELREEGHGDKKDEPWPMPKMTVQELIDSCITITIWIASALHAAVN 718

Db 659 SDELVLKDNELQAWKELREEGHGDKKDEPWPMPKMTQRELKDSCTIIIIWIASALHAAVN 718

QY 719 FGQYPYAGYLPNRPTLSRNFMPPEPGSPSEYEELKTNPDKVFLKTTIPQLQTLIGISLIEL 778

Db 719 FGQYPYAGYLPNRPTLSRRFMPEPGTPEYEELKTNPDKAYLKTITPQLQTLIGISLIEL 778

QY 779 SRHSSDTLYLQGRESPEWTKDQEPLSAFARFGKLSIEDIQIMQNVNDEKWNRSRGPVKV 838

Db 779 SRHASDEIYLGQRDSSEWTKDQEPAAAFERFGKLSIEDQIIQWNGDKKWNRSRGPVNV 838

QY 839 PYTLLFPTSEGGLTGKIPNSVSI 862

Db 839 PYTLLFPTSEGLTGKIPNSVSI 862





CC		hydroperoxyoctadeca-9,11-dienoate.	
CC	-!	COFACTOR: Iron (By similarity).	
CC	-!	SIMILARITY: Belongs to the lipoxxygenase family.	
CC	-!	SIMILARITY: Contains 1 PLAT domain.	
DR	EMBL; AY254347;	AAP83136.1; -.	
DR	EMBL; AY254345;	AAP83134.1; -.	
DR	GO; GO:0005506;	F:iron ion binding; IEA.	
DR	GO; GO:0016165;	F:lipoxxygenase activity; IEA.	
DR	GO; GO:0016491;	F:oxidoreductase activity; IEA.	
DR	GO; GO:0006118;	P:electron transport; IEA.	
DR	InterPro; IPR000907;	Lipoxxygenase.	
DR	InterPro; IPR001024;	Lipoxxygenase_LH2.	
DR	InterPro; IPR001246;	Plant_lipoxygense.	
DR	InterPro; IPR008976;	PLAT_LH2.	
DR	Pfam; PF00305;	Lipoxxygenase; 1.	
DR	Pfam; PF01477;	PLAF; 1.	
DR	PRINTS; PR00087;	LIPPOXYGENASE.	
DR	PRINTS; PR00468;	PLTLPOXGNASE.	
DR	SMART; SM00308;	LH2; 1.	
DR	PROSITE; PS00711;	LIPPOXYGENASE_1; 1.	
DR	PROSITE; PS00081;	LIPPOXYGENASE_2; 1.	
DR	PROSITE; PS50095;	PLAT; 1.	
KW		Dioxygenase; Oxidoreductase.	
SQ	SEQUENCE	861 AA; 97214 MW; 50EBE9BD8420D6ED CRC64;	
Query Match 84.2%; Score 3816.5; DB 2; Length 861;			
Best Local Similarity 81.7%; Pred. No. 8.6e-246;			
Matches 705; Conservative 81; Mismatches 74; Indels 3; Gaps 3;			
QY	1	MF-LEKIVDAITGDKGKKVGTVLMKKNVLDFTDINASVLGVLFLGRRVLSLELISS	59
Db	1	MFPIKNIVDGLIGHNDSKKVKGIVVMKKNALDFTDIAGAVDGVLEFVGQKVSQLISS	60
QY	60	VNADPANGLOQKRSKAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHF	119
Db	61	AHGDPAANDLOQKHSNPAYLENWLTITITLTAGESAYGVTFDW-DEEFGLPGAFIKNLHF	119
QY	120	SEFFLKSLTLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYREN	179
Db	120	TEFFLKSVTLEDVPHNGTVHVCNSWVYPANKYKSDRIFFANKTYLPSETPAPLLKYREN	179
QY	180	ELVTLRGDGTGKLEEDWRVYDYAYVNDLGDPPDKGQDLSRPVLGGSSEYPYPRRGRTRKP	239
Db	180	ELLTLRGDGTGKLEAWDRVYDYALYNDLGDPPDQGAQHVRPILGGSSDYPYPRRGRTRAP	239
QY	240	TKTDPNSESRIPLMSLDIYVPRDERFGHFKLSDFLTALKSIVQLLPEFKALFDSTHN	299
Db	240	TRTDPESERIPLLSLDIYVPRDERFGHLKLSDFLTALKSMVQFILPELHALFDSTPN	299
QY	300	EFDSFEDVLKLYEGGIKLPGQPLLKAITSDIPLEILKELLRSDEGELFKYPTPQVIOEDK	359
Db	300	EFDSFEDVLRLYEGGIKLPGQPLFKALISSIPLEVMVKELLRTDGEIGMKFPTPLVIKEDK	359
QY	360	TAWRTDEEFGREMLAGVNPVVISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTI	419
Db	360	TAWRTDEEFGREMLAGVNPVVIIRNLQEFPPKSKLDPQVYGNQDSTITIQHIEDRLDGLTI	419
QY	420	DEAIKTNRLFILNHHDLMPYLRRINTSTDTKTYASRTLFLQDNGTLKPSAIELSLPHP	479
Db	420	DEAIKSNRLFILNHHDTIMPYLRRINTTT-TKTYASRTLFLQDNGCLKPLAIELSLPHP	478
QY	480	DGQDFGAVSKVYTPADQGVESIWQLAKAYAANDSGVHQLISHWLNTHAAIEPFVIATN	539
Db	479	DGQDFGALSIVYTPDEGVEGSIWELAKAYAVANDSGVHQLISHWLNTHAVIEPFVIATN	538
QY	540	ROLSALHPITKLLHPHFRETMINALARQIILNGGLLELTVPFPAKYSMEMSAVVYKDW	599
Db	539	ROLSVLHPITKLLHPHFRDTMINAMARQIILINAGGVLESTVPFPSKYAMEMSAVVYKNWI	598
QY	600	FPEQALPTDLIKRGVAVEDSSSPGLIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKS	659
Db	599	FPDQALPTDLVKGMAVEDSSSPHGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCSFYKS	658
QY	660	DDAVQKDTLQAWWKELREEGHGDKDEPWPKMQTVQELIDSCITITIIWIASALHAAVNF	719
Db	659	DDSILKDNELQAWWKELREEGHGDLKDEPWPKMENCQELIDSCITIIWTASALHAAVNF	718
QY	720	GQYPYAGYLPNRPRTLNRNFMPEPGSPYEELKTNPDKVFLLKTITPQLQTLGLISLIEILS	779
Db	719	GQYPYAGYLPNRPRTVSRFRMPEPGTSEYELLKTNPDKAFRLTITTAQLQTLGLVSLIEILS	778
QY	780	RHSSDTLYLQORESPETWKDQEPLSAFARFGKKLSDIEDQIQMNVDEKWKNRSGPVKVP	839
Db	779	RHTSDEIYLGORDSPKWTYDEEPLAADFPGNKLSDIENRIIEMNGDQIWRNRSGPVKAP	838
QY	840	YTLFPPTSEGGLTGKIPNSVSI	862
Db	839	YTLFPPTSEGGLTGKGVPSVSI	861
RESULT 6			
Q41238		PRELIMINARY;	PRT; 857 AA.
ID	Q41238		
AC	Q41238;		
DT	01-NOV-1996 (TReMBLrel. 01, Created)		
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	Linoleate:oxygen oxidoreductase (Fragment).		
OS	Solanum tuberosum (Potato).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;		
OC	lamids; Solanales; Solanaceae; Solanum.		
OX	NCBI_TaxID=4113;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94302170; PubMed=8029354; DOI=10.1104/pp.105.1.269;		
RA	Geerts A., Feltkamp D., Rosahl S.;		
RT	"Expression of lipoxxygenase in wounded tubers of Solanum tuberosum		
RT	L.";		
RL	Plant Physiol. 105:269-277(1994).		
CC	-!	FUNCTION: plant lipoxxygenase may be involved in a number of	
CC		diverse aspects of plant physiology including growth and	
CC		development, pest resistance, and senescence or responses to	
CC		wounding (By similarity).	
CC	-!	CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-	
CC		hydroperoxyoctadeca-9,11-dienoate.	
CC	-!	COFACTOR: Iron (By similarity).	
CC	-!	SIMILARITY: Belongs to the lipoxxygenase family.	
CC	-!	SIMILARITY: Contains 1 PLAT domain.	
DR	EMBL; S73865;	AAB31252.1; -.	
DR	HSSP; P08170;	1FGT.	
DR	GO; GO:0005506;	F:iron ion binding; IEA.	
DR	GO; GO:0016165;	F:lipoxxygenase activity; IEA.	
DR	GO; GO:0016491;	F:oxidoreductase activity; IEA.	
DR	GO; GO:0006118;	P:electron transport; IEA.	
DR	InterPro; IPR000907;	Lipoxxygenase.	
DR	InterPro; IPR001024;	Lipoxxygenase_LH2.	
DR	InterPro; IPR001246;	Plant_lipoxygense.	
DR	InterPro; IPR008976;	PLAT_LH2.	
DR	Pfam; PF00305;	Lipoxxygenase; 1.	
DR	Pfam; PF01477;	PLAT; 1.	
DR	PRINTS; PR00087;	LIPPOXYGENASE.	
DR	PRINTS; PR00468;	PLTLPOXGNASE.	
DR	SMART; SM00308;	LH2; 1.	
DR	PROSITE; PS00711;	LIPPOXYGENASE_1; 1.	
DR	PROSITE; PS00081;	LIPPOXYGENASE_2; 1.	
DR	PROSITE; PS50095;	PLAT; 1.	
KW		Dioxygenase; Oxidoreductase.	
FT	NON TER	857; 857	
SQ	SEQUENCE	857 AA; 96585 MW; 3785A24E8DBA8DA7 CRC64;	
Query Match 81.5%; Score 3695; DB 2; Length 857;			
Best Local Similarity 80.0%; Pred. No. 1.1e-237;			
Matches 682; Conservative 84; Mismatches 85; Indels 2; Gaps 2;			
QY	10	ITGKDDGKKVGTVLMKKNVLDFTDINASVLGVLFLGRRVLSLEISSVNADPANGLO	69

Db 7 IGGHDSKKVKGTVVMKKNALDFTDLAGSLTDKIFEALGQKVSFQLISSVQSDPANGLO 66

Qy 70 GKRSKAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHSEFFLKSRTL 129

Db 67 GKHSNPAYLENFLTLTPLAAGETAFTGVTFDW-NEEFGVPGAFIKNTHINEFFLKSRTL 125

Qy 130 EDVPHGKVHVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELVTLRGDGT 189

Db 126 EDVPHGKVHVCNSWVYPSFRYKSDRIFFANQAYLPSETPELLRKYRENELLTLRGDGT 185

Qy 190 GKLEWDRVYDYAYNDLGDGQDLSPVLGGSSEYPYPRRGRTGRKPTKTDPNSES 249

Db 186 GKREAWDRIYDYVNDLGNPDQGEQNVRTTLGGSADYPYPRRGRTGRPTRTDPKSES 245

Qy 250 IPLLMSLDIYVPRDERFCHIKLSDFLTFALKSIVQLLPBPKALFDSTHNEFDSFEDVLK 309

Db 246 IPLLMSLDIYVPRDERFCHIKLSDFLTFALKSIVQFILPELHALFDGTPNEFDSFEDVLR 305

Qy 310 LYEGGIKLPQGPLLKAITDSIPLEILKELLRSDEGLFKYPTPQVIOEDKTAWRTDEEFG 369

Db 306 LYEGGIKLPQGPLFKALTAAPLEMKELLRTDGEGLRPPTPLVIKOSKTAWRTDEEFA 365

Qy 370 REMLAGVNPVIIISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKTNRLF 429

Db 366 REMLAGVNPVIIISRLQEFPPKSKLDPEAYGNQNSTITAETHIEDKLDGLTVDEAMNNKLF 425

Qy 430 ILNHHDILMPYLRRINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPHPDGQFGAVSK 489

Db 426 ILNHHDVLIPLYLRINTTT-TKTYASRTLLFLQDNGSLKPLAIELSLPHPDGQFGVTSK 484

Qy 490 VYTPADQGVESIWOLAKAYAVNDSGVHQLISHWLNTHAAIEFPFVIATNRQLSALHPIY 549

Db 485 VYTPSDQGVESIWOLAKAYAVNDSGVHQLISHWLNTHAVIEFPFVIATNRQLSVLHPIH 544

Qy 550 KLLHPHFRETMINALARQIILNGGELLELTVPFAKYSMENSAVVYKDWVPPEQALPTDL 609

Db 545 KLLYPHFRDTMINAMARQIILINAGGVLESTVPFSKFAMENSAVVYKDWVFPDQALPADL 604

Qy 610 IKGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWTETVCNYYKSDDAVQKDTL 669

Db 605 VKRGVAVEDSSSPHGVRLLIEDYPYAVDGLEIWSAIKSWVTDYCSFYGSDEEILKDNE 664

Qy 670 QAWKELREEGHGDKKDEPWPKNQTVQELIDSCITITWIASALHAANVFGQPYAGYLP 729

Db 665 QAWKELREVGHGDKKNPWPPEMETPQELIDSCITIIWIASALHAANVFGQPYAGYLP 724

Qy 730 NRPTLSRNFMPPEGSPYEELKTNPDKVFLKTIPTQLQTLGLTSLIEILSRHSSDTLYLG 789

Db 725 NRPTVSRFMPPEGTPYEELKKNPDKAFKTIITAQLQTLGLVSLIEILSRHTTDEIYLG 784

Qy 790 QRESPENTKQEPPLSAFARFGKKLSDIEDQIMQMVNDEKWKNRSGPVKVPYTLFFPTSEG 849

Db 785 QRESPENTKQEPPLAFAFDKFGKLLTDIEKQIIQRNGDNILTNRSGPVNAPYTLFFPTSEG 844

Qy 850 GLTGKIPNSVSI 862

Db 845 GLTGKIPNSVSI 857

RESULT 7

Q43190

ID Q43190 PRELIMINARY; PRT; 860 AA.

AC Q43190;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Lipoxigenase (EC 1.13.11.12).

GN Name=PTLX-2;

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

QC lamiiids; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=41113;

RN [1]

RP SEQUENCE FROM N.A.

RA Kolomiets M.V., Hannapel D.J., Gladon R.J.;

RT "Potato Lipoxigenase Genes Expressed During the Early Stages of

RT Tubertization (Accession Nos. U60200 and U60201) (PGR96-065).";

RL Plant Physiol. 112:446-446(1996).

CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of

CC diverse aspects of plant physiology including growth and

CC development, pest resistance, and senescence or responses to

CC wounding (By similarity).

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron (By similarity).

CC -!- SIMILARITY: Belongs to the lipoxigenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

DR EMBL; U60201; AAB67860.1; -.

DR HSSP; P08170; 1FGT.

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0016165; F:lipoxigenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000907; Lipoxigenase.

DR InterPro; IPR001024; Lipoxigenase\_LH2.

DR InterPro; IPR001246; Plant\_lipoxynse.

DR InterPro; IPR008976; PLAT\_LH2.

DR Pfam; PF00305; Lipoxigenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PR00087; LIPOXYGENASE.

DR PRINTS; PR00468; PLTLPOXGNASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.

DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.

DR PROSITE; PS50095; PLAT; 1.

KW Dioxigenase; Oxidoreductase.

SQ SEQUENCE 860 AA; 96968 MW; 11FD0D769921053E CRC64;

Query Match 81.5%; Score 3693; DB 2; Length 860;

Best Local Similarity 79.8%; Pred. No. 1.5e-237;

Matches 681; Conservative 86; Mismatches 84; Indels 2; Gaps 2;

Qy 10 ITGKDDGKKVKGTVVLMKKNVLDFTDINASVLDGVLEFLGRRVSLELISSVNADPANGLO 69

Db 10 IGGHDSKKVKGTVVMKKNALDFTDLAGSLTDKIFEALGQKVSFQLISSVQSDPANGLO 69

Qy 70 GKRSKAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHSEFFLKSRTL 129

Db 70 GKHSNPAYLENFLTLTPLAAGETAFTGVTFDW-NEEFGVPGAFIKNTHINEFFLKSRTL 128

Qy 130 EDVPHGKVHVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELVTLRGDGT 189

Db 129 EDVPHGKVHVCNSWVYPSFRYKSDRIFFANQAYLPSETPELLRKYRENELLTLRGDGT 188

Qy 190 GKLEWDRVYDYAYNDLGDGQDLSPVLGGSSEYPYPRRGRTGRKPTKTDPNSES 249

Db 189 GKREAWDRIYDYVNDLGNPDQGEQNVRTTLGGSADYPYPRRGRTGRPTRTDPKSES 248

Qy 250 IPLLMSLDIYVPRDERFCHIKLSDFLTFALKSIVQLLPBPKALFDSTHNEFDSFEDVLK 309

Db 249 IPLLMSLDIYVPRDERFCHIKLSDFLTFALKSIVQFILPELHALFDGTPNEFDSFEDVLR 308

Qy 310 LYEGGIKLPQGPLLKAITDSIPLEILKELLRSDEGLFKYPTPQVIOEDKTAWRTDEEFG 369

Db 309 LYEGGIKLPQGPLFKALTAAPLEMIRELLRTDGEGLRPPTPLVIKOSKTAWRTDEEFA 368

Qy 370 REMLAGVNPVIIISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKTNRLF 429

Db 369 REMLAGVNPVIIISRLQEFPPKSKLDPEAYGNQNSTITAETHIEDKLDGLTVDEAMNNKLF 428

Qy 430 ILNHHDILMPYLRRINTSTDTKYASRTLLFLQDNGTLKPSAIELSLPHPDGQFGAVSK 489

Db 429 ILNHHDVLIPLYLRINTTT-TKTYASRTLLFLQDNGSLKPLAIELSLPHPDGQFGVTSK 487





Db 668 QAWWKEVREVGHGDKGNPPWAAEMETPQELIDSCCTIIWIASALHAAVNFQGYPYAGYLP 727

Qy 730 NRPTLSRNFMPPEPGSPYEELKTNPDKVFLKTTIPQLQTLGLGISLIEILSRHSSDTLYLG 789

Db 728 NRPTVSRKFMPEPGTPYEELKKNPDKAFKKTITAQLQTLGLVSLIEILSRHTTDEIYLG 787

Qy 790 QRESPWTKDQEPLSAFARFGKLLSDIEDQIMQMVNDEKWKNSRGPVKVPYTLFLFPTSEG 849

Db 788 QRESPWTKDKEPLAFAFERFGNKLTDIEKQIMQRNGNNILNTRGPNAPYTLFLFPTSEG 847

Qy 850 GLTGKIPNSVSI 862

Db 848 GLTGKIPNSVSI 860

RESULT 9

O24379 PRELIMINARY; PRT; 861 AA.

AC O24379;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Lipoxigenase (EC 1.13.11.12).

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamids; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4113;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tuber;

RX MEDLINE=96355454; PubMed=8702864; DOI=10.1074/jbc.271.35.21012;

RA Royo J.N., Vancanneyt G., Perez A.G., Sanz C., Stormann K., Rosahl S.,

RA Sanchez-Serrano J.J.;

RT "Characterization of three potato lipoxigenases with distinct

RT enzymatic activities and different organ-specific and wound-regulated

RT expression patterns.";

RL J. Biol. Chem. 271:21012-21019(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Tuber;

RA Royo J.;

RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of

CC diverse aspects of plant physiology including growth and

CC development, pest resistance, and senescence or responses to

CC wounding (By similarity).

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron (By similarity).

CC -!- SIMILARITY: Belongs to the lipoxigenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

DR EMBL; X95513; CAA64766.1; -.

DR HSSP; P08170; 1FGT.

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0016165; F:lipoxigenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000907; Lipoxigenase.

DR InterPro; IPR001024; Lipoxigenase\_LH2.

DR InterPro; IPR001246; Plant\_lipoxynase.

DR InterPro; IPR008976; PLAT\_LH2.

DR Pfam; PF00305; Lipoxigenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PR00087; LIPOXYGENASE.

DR PRINTS; PR00468; PLTLPXGNASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.

DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.

DR PROSITE; PS50095; PLAT; 1.

KW Dioxxygenase; Oxidoreductase.

SEQUENCE 861 AA; 97066 MW; 25783F32C69BFA26 CRC64;

Query Match 80.4%; Score 3643.5; DB 2; Length 861;

Best Local Similarity 79.2%; Pred. No. 3e-234;

Matches 675; Conservative 82; Mismatches 92; Indels 3; Gaps 3;

Qy 12 GKDDGKKVGTVLMKKNVLDFTDINASVLGVLGFLGRRVSLELISSVNADPANGLOGK 71

Db 12 GPDDSKKLKGTVMNMKNALDFTDLAGSLTDKAPEFLGQTVSFQLISSVQGDPTNGLQK 71

Qy 72 RSKAAYLENWLTNSTPIAAG-ESAFRVTFDWDDEEFGVPGAFIKNLHSEFFLKSLTLE 130

Db 72 HSNPAYLENSLFTLTPLTAGSETAFGVTFDW-NEEFGVPGAFIKNTHINEFFLKSLTLE 130

Qy 131 DVPNHGKVHFCVNSWVYPANKYKSDRIFFPANQAYLPSETDTLRKYRENELVTLRGDGTG 190

Db 131 DVPNHGKVHFCVNSWVYPSFRYKSDRIFFNQPYLPSPKTPPELLRKYRENELTLRGDGTG 190

Qy 191 KLEWDRVYDYAYYNDLGDPDKGQDLSPVLGGSSEYYPRRGRTRGKPTKTDPNSESRI 250

Db 191 KREAWDRIYDYIYNDLGNDEGKENVRTTLGSAEYPYPRRGTRGPTRTDPKSESRI 250

Qy 251 PLLMSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLPEFKALFDSTHNEFDSFEDVLKL 310

Db 251 PLILSLDIYVPRDERFGHLKMSDFLYALKSIVQFILPELHALFDGTPNEFDSFEDVLR 310

Qy 311 YEGGIKLPOGPLLKAITDSTPLEILKELLRSDEGELFKYKPTQVQIEDKTAWRTDEEFG 370

Db 311 YEGGIKLPOGPLFKALTAALPLEMIRELLRTDGEGLRFPPLVIKDSKTAWRTDEEFAR 370

Qy 371 EMLAGVNPVVISRLQEFFPKSKLDPKIYGNQNSTITRETIQIEDKLDGLTIDEAIKTNLFI 430

Db 371 EMLAGVNPVVISRLQEFFPKSKLDPEAYGNQNSTITAETHIEDKLDGLTVDEAMNNKLF 430

Qy 431 LNHHDLMPYLRRINTSTDTKTYASRTLLEFLQDNGTLKPSAIELSLPHPDGDQFGAVSKV 490

Db 431 LNHHDLIPYLRRINTTT-TKTYASRTLLEFLQDNGSLKPLAIELSLPHPDGDQFGVTSKV 489

Qy 491 YTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQLSALHPIYK 550

Db 490 YTPSDQGVESIWQLAKAYAVNDSGVHQLISHWLNTHAVIEPFVIATNRQLSVLHPIHK 549

Qy 551 LLHPHFRETMINALARQILINGGGLLELTVFPKYSMEMSAVVYKDWVPFEQALPTDLI 610

Db 550 LLYPHFRDTMINAMARQILINAGGVLESTVFQSKFAMEMSAVVYKDWVFPDQALPADLV 609

Qy 611 KRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWTTEYCNYYKSDDAVQKDTELQ 670

Db 610 KRGVAVEDSSSPHGVRLIEDYPYAVDGLEIWSAIKSWSDYCSFYYSDEEILKDNELO 669

Qy 671 AWWKELREEGHGDKKDEPWPVKQTVQELIDSCCTITTIWIASALHAAVNFQGYPYAGYLPN 730

Db 670 AWWKELREVGHGDKKNEPWPWEMERPQELIDSCCTIIWIASALHAAVNFQGYPYAGYLPN 729

Qy 731 RPTLSRNFMPPEPGSPYEELKTNPDKVFLKTTIPQLQTLGLGISLIEILSRHSSDTLYLQ 790

Db 730 RPTVSRRFMPPEPGTPEYEELKKNPDKAFKKTITAQLQTLGLVSLIEILSRHTTDEIYLG 789

Qy 791 RESPEWTKDQEPLSAFARFGKLLSDIEDQIMQMVNDEKWKNSRGPVKVPYTLFLFPTSEG 850

Db 790 RESPEWTKDKEPLAFAFDKFGKLLTDIEKQIIQRNGDNILNRSRGPVNAPYTLFLFPTSEG 849

Qy 851 LTGKGIPNSVSI 862

Db 850 LTGKGIPNSVSI 861

RESULT 10

Q9SC16

ID Q9SC16 PRELIMINARY; PRT; 861 AA.

AC Q9SC16;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Lipoxigenase (EC 1.13.11.12).

[illegible]

Db	311	YEGGIKLPQGFALFKALTAAPLEMIKRELLRTDGEIGILRFPPTPLVTKDSKTAWRTDEEFAR	371
Qy	371	EMLAGVNPVIIISRLQEFPPKSLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKTNRLFI	430
Db	371	EMLAGVNPVIIISRLQEFPPKSLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKTNRLFI	430
Qy	431	LNHHDILMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPDGQFGAVSKV	490
Db	431	LNHHDVILPYLRRINT-TITKTYASRTLLFLQDNGSLKPLAIELSLPHPDGQFGVTSKV	489
Qy	491	YTPADQGVESIWQLAKAYAVNDSGVHQLISHWLNTAAIEPFVIATNRQLSALHPIYK	550
Db	490	YTPSDQGVESIWQLAKAYAVNDTGVLHQLISHWLNTAAIEPFVIATNRQLSVLHPIHK	549
Qy	551	LLHPHFRETMINALARQILLINGGGLLELTVFPKYSMEMSAVVYKDWVFPPEQALPTDLI	610
Db	550	LLYPHFRTMINASARQILVNAGGVLESTVFQSKFAMEMSAVVYKDWVFPDQALPADLV	609
Qy	611	KRGVAVEDSSSPGLIRLLIQDYPYAVDGLKIWSAISKSWTVEYCNVYKSDDAVQKDTLQ	670
Db	610	KRGVAVEDSSSPHGVRLIEDYPYAVDGLKIWSAISKSWTVEYCNVYKSDDEILKDNELQ	669
Qy	671	AWKELREEGHGDKDEPWPKQTVQELIDSCITTIWIASALHAAVNFQYPIYAGYLPN	730
Db	670	AWKELREVGHGDKNEPWPPEMKTQPELIDSCITTIWIASALHAAVNFQYPIYAGYLPN	729
Qy	731	RPTLSRNFMEPGSPYEELKTNPKVFLKTIPTQLQTLGLISLIEILSRHSSDTLYLQ	790
Db	730	RPTVSRRFMEPGTDPYELKRNPKAFKTIITAQLQTLGLISLIEILSRHTTDEIYLGQ	789
Qy	791	RESPEWTKDQEPLSAFARFGKKLSIEDQIMQNVDEKWKNRSGPVKVPTLLFPTSEGG	850
Db	790	RESPEWTKDKEPLAADFDFGKKLTDEKQIIQRNGDNILTNRSGPVNAPYTLFPTSEGG	849
Qy	851	LTGKGIPNSVSI 862	
Db	850	LTGKGIPNSVSI 861	

RESULT 11

O22508 PRELIMINARY; PRT; 861 AA.

AC O22508;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Lipoxigenase.

GN Name=plox2;

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4113;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Lehmi Russet; TISSUE=Tuber;

RA Fidantsef A.L., Bostock R.M.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of

CC diverse aspects of plant physiology including growth and

CC development, pest resistance, and senescence or responses to

CC wounding (By similarity).

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron (By similarity).

CC -!- SIMILARITY: Belongs to the lipoxigenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

DR EMBL; AF019614; AAB81595.1; -

DR HSSP; P08170; 1FGT.

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0016165; F:lipoxigenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.





Db 134 DVPNHGKVHFDNCNSWVYPSFRYKSDRIFFANQPYLPSKTPPELLRKYRENEELLTLRGDGTG 193

Qy 191 KLEWDRVYDYAYNDLGDPPDKGQDLSRPVLGSGSEYYPYRRGRTGRKPTKTDPNSESRI 250

Db 194 KREAWDRYDYDIYNDLGNPDQGENVRTTLGSAEYYPYRRGRTGRPTRTDPKSESRI 253

Qy 251 PLLMSLDIYVPRDERFGHIKLSDFLTFALKSTVQLLPEFKALFDSHNEFDSFEDVLKL 310

Db 254 PLLSLDIYVPRDERFGHLKMSDFLTALYALKSVQFILPELHALFDGTNEFDSFEDVLR 313

Qy 311 YEGGIKLPQGLPKAITDSIPLEILKELRSDEGLFKYPTQVQIQEDKTAWRTDEEFGR 370

Db 314 YEGGIKLPQGLPKAITAAIPLEMIKELRTDGEILRFTPLVIKDSKTAWRTDEEFAR 373

Qy 371 EMLAGVNPVIISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIAKTNRLFI 430

Db 374 EMLAGVNPVIISRLQEFPPKSKLDPEAYGNQNSTITAEHIEDKLDGLTVDEAMNNKLF 433

Qy 431 LNHHDLMPYLRINTSTDTKYASRTLLFQDNGTLKPSAIELSLPHPDGDQFGAVSKV 490

Db 434 LNHHDLIPYLRINT-TITKSYASRTLLFQDNGSLKPLAIELSLPHPDGDQFGVTSKV 492

Qy 491 YTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTAAIEPFVIATNRQLSALHPIYK 550

Db 493 YTPSDQGVESIWQLAKAYAVNDAGVHQLISHWLNTHAVIEPFVIATNRQLSVLHPIK 552

Qy 551 LLHPHRETWMNALARQILINGGLLELTVPKAYSMEMSAVVYKDWVPEQALPTDLI 610

Db 553 LLYPHFRDTWMNARSARQILINAGGVLESTVFQSKFALEMSAVVYKDWVFPDQALPADLV 612

Qy 611 KRGVAVEDSSPLGIRLLIODYPYAVDGLKIWSAISKSWTTEYCNYYKSDDAVQKDTLQ 670

Db 613 KRGVAVEDSSPHGVRLLIEDYPYAVDGLKIWSAISKSWTDYCSFYGSDEEILKDNELQ 672

Qy 671 AWWKELREHGDKKDEPWPMQMTVOELIDSCITITIIWIASALHAANFGQYPYAGYLPN 730

Db 673 AWWKELREVGHDGKKNPWPEMETPQELIDSCITITIIWIASALHAANFGQYPYAGYLPN 732

Qy 731 RPTLSRNFPEPGSPYEELKTNPKVFLKTIPTQLTLGSLIELLSRHSSDLYLQ 790

Db 733 RPTVSRRFPEPGTPEYEELKKNPKDKAFKLTITAQLTLGSLVELLSRHTTDEIYLQ 792

Qy 791 RESPEWTKDQPLSAFARFGKLSDIEDQIMQMNVDKWKNSRGPVKVPYTLFFPTSEGG 850

Db 793 RESPEWTKDKEPLAADFCKGKLTIDIEKQIIQRNGDNILNRSRGPVNAPYTLFFPTSEGG 852

Qy 851 LTGKGIPNSVSI 862

Db 853 LTGKGIPNSVSI 864

RESULT 13

LOX1 SOLTU

ID LOX1 SOLTU STANDARD; PRT; 861 AA.

AC P37831;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Lipoxigenase 1 (EC 1.13.11.12).

GN Name=LOX1.1; Synonyms=LOX1;

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4113;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Desiree; TISSUE=Tuber;

RX MEDLINE=95175602; PubMed=7870815; DOI=10.1104/pp.107.1.265;

RA Casey R.;

RT "Sequence of a cDNA clone encoding a potato (Solanum tuberosum) tuber

RT lipoxigenase.";

RL Plant Physiol. 107:265-266 (1995).

CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of

CC diverse aspects of plant physiology including growth and

CC development, pest resistance, and senescence or responses to

CC wounding. It catalyzes the hydroperoxidation of lipids, containing

CC a cis,cis-1,4-pentadiene structure.

CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-

CC hydroperoxyoctadeca-9,11-dienoate.

CC -!- COFACTOR: Iron, one atom tightly bound per molecule.

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the lipoxigenase family.

CC -!- SIMILARITY: Contains 1 PLAT domain.

CC -----

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CC -----

DR EMBL; X79107; CAA55724.1; --

DR PIR; S44940; S44940.

DR HSSP; P08170; 1FGT.

DR InterPro; IPR000907; Lipoxigenase.

DR InterPro; IPR001024; Lipoxigenase LH2.

DR InterPro; IPR001246; Plant\_lipoxynase.

DR InterPro; IPR008976; PLAT\_LH2.

DR Pfam; PF00305; Lipoxigenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PR00087; LIPOXYGENASE.

DR PRINTS; PR00468; PLTLPXGNASE.

DR SMART; SM00308; LH2; 1.

DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.

DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.

DR PROSITE; PS50095; PLAT; 1.

DR DiOxygenase; Iron; Multigene family; Oxidoreductase.

KW

FT DOMAIN 29 160 PLAT.

FT METAL 522 522 Iron (By similarity).

FT METAL 527 527 Iron (By similarity).

FT METAL 713 713 Iron (By similarity).

FT METAL 861 861 Iron (By similarity).

SQ SEQUENCE 861 AA; 96966 MW; 09732A6751DEE20D CRC64;

Query Match 80.1%; Score 3632.5; DB 1; Length 861;

Best Local Similarity 78.9%; Pred. No. 1.7e-233;

Matches 672; Conservative 83; Mismatches 94; Indels 3; Gaps 3;

Qy 12 GKDDGKKVKGTVVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLELISSVNADPANGLOGK 71

Db 12 GHDDSKKVKGTVVMMKNVLDFTDLAGSLTGKIFDVLGQKVSFQLISSVQGDPTNGLQK 71

Qy 72 RSKAAYLENWLTNSTPIAAG-ESAFRVTFDWDDEEFGVPGAFIKNLHSEFFLKSLTLE 130

Db 72 HSNPAYLENSLFTLTPLTAGSETAFGVTFDW-NEEFGVPGAFIKNMHINEFFLKSLTLE 130

Qy 131 DVPNHGKVHFCNSWVYPANKYKSDRIFFANQAYLPSETPTLTKYRENEELVTLRGDGTG 190

Db 131 DVPNHGKVHFCNSWVYPSLNYKSDRIFFANQAYLPSETPELLRKYRENEELLTLRGDGTG 190

Qy 191 KLEWDRVYDYAYNDLGDPPDKQDLSRPVLGSGSEYYPYRRGRTGRKPTKTDPNSESRI 250

Db 191 KREAWDRYDYDIYNDLGNPDQGENVRTTLGSAEYYPYRRGRTGRPTRTDPKSESRI 250

Qy 251 PLLMSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLPEFKALFDSHNEFDSFEDVLKL 310

Db 251 PLLSLDIYVPRDERFGHLKMSDFLTALYALKSIVQFILPELHALFDGTNEFDSFEDVLR 310

Qy 311 YEGGIKLPQGLPKAITDSIPLEILKELRSDEGLFKYPTQVQIQEDKTAWRTDEEFGR 370

Db 311 YEGGIKLPQGLPKALTAAIPLEMIKELRTDGEILRFTPLVIKDSKTAWRTDEEFAR 370

Qy 371 EMLAGVNPVIISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIAKTNRLFI 430

Db 371 EMLAGVNPVILSRLOEFPKSKLDPEAYGNQNSTITAETHIEDKLDGLTVDEAMNNKULFI 430  
Qy 431 LNHHDLMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHDPGDQFGAVSKV 490  
Db 431 LNHHDVIIPLYLRRINT-TITKAYASRTLLFLQDNGSLKPLAIELSFPHDPGDQFGVTSKV 489  
Qy 491 YTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFFVIATNRQLSALHPYIK 550  
Db 490 YTPSDQGVESSIWQLAKAYAVNDGVGHQLISHWLNTHAVIEPFFVIATNRQLSVLHPHK 549  
Qy 551 LLHPHFRETMINALARQILINGGGLLELTVFPAKYSMEMSAVVYKDWVFEQALPTDLI 610  
Db 550 LLYPHFRDTMINASARQLLVNAGGVLESTVFQSKFAMEMSAVVYKDWVFPDQALPADLV 609  
Qy 611 KRGVAVEDSSSPLGIRLLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKSDDAVQKDTLQ 670  
Db 610 KRGVAVEDSSSPHGVRLIEDYPIYAVDGLIWSAIKSWVTDYCSFYGSDDEILKDNELQ 669  
Qy 671 AWWKELREEGHGDKKDEPWPWKMTQVQELIDSCCTIITIIWIASALHAAVNFQYPYAGYLPN 730  
Db 670 AWWKELREVGHDGDKKNEPWPPEMETPQELIDSCCTIITIIWIASALHAAVNFQYPYAGYLPN 729  
Qy 731 RPTLSRNPPEPGSPESYEELKTNPKVFLKTIPTQLOTLGLGISLIEILSRHSSDTLYLGQ 790  
Db 730 RPTVSRRPPEPGTPEYEELKRNPKAFKLTITAQLQTLGVSILVEILSRHTTDEIYLGQ 789  
Qy 791 RESPEWTKDQPLSAFARFGKKLSLIEDQIMQMNVDKWKNRSGPVKVPYTLFLFPTSEGG 850  
Db 790 RESPEWTKDKEPLAADFRTGKLLTDIEKQIIQRNGDNILTNRSQPNAPYTLFLFPTSEGG 849  
Qy 851 LTGKGIPNSVSI 862  
Db 850 LTGKGIPNSVSI 861

RESULT 14  
Q42873  
ID Q42873 PRELIMINARY; PRT; 859 AA.  
AC Q42873;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Lipoxigenase (EC 1.13.11.12).  
GN Name=LOX;  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Iamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rutgers; TISSUE=Fruit pericarp;  
RX MEDLINE=95241637; PubMed=7724686; DOI=10.1104/pp.107.2.669;  
RA Kausch K.D., Handa A.K.;  
RT "Molecular cloning and nucleotide sequence of a lipoxigenase cDNA from  
RT ripening tomato fruit."  
RL Plant Physiol. 107:669-670(1995).  
CC -!- FUNCTION: Plant lipoxigenase may be involved in a number of  
CC diverse aspects of plant physiology including growth and  
CC development, pest resistance, and senescence or responses to  
CC wounding (By similarity).  
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-  
CC hydroperoxyoctadeca-9,11-dienoate.  
CC -!- COFACTOR: Iron (By similarity).  
CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
CC -!- SIMILARITY: Contains 1 PLAT domain.  
DR EMBL; U13681; AAA74393.1; -.  
DR PIR; T06352; T06352.  
DR HSSP; P09186; INO3.  
DR GO; GO:0005506; F:Iron ion binding; IEA.  
DR GO; GO:0016165; F:lipoxigenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR000907; Lipoxigenase.  
DR InterPro; IPR001024; Lipoxigenase\_LH2.  
DR InterPro; IPR001246; Plant\_lipoxynse.  
DR InterPro; IPR008976; PLAT\_LH2.  
DR Pfam; PF00305; Lipoxigenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR PRINTS; PR00468; PLTLPOXGNASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS50095; PLAT; 1.  
KW Dioxygenase; Oxidoreductase.  
SQ SEQUENCE 859 AA; 97136 MW; 738DE7E070A793C8 CRC64;  
  
Query Match 80.0%; Score 3625.5; DB 2; Length 859;  
Best Local Similarity 79.4%; Pred. No. 4.8e-233;  
Matches 685; Conservative 70; Mismatches 103; Indels 5; Gaps 3;  
  
Qy 1 MFLEKIVDAITGKDDGKKVGTVVLMKKNVLDFTDINASVLDGVLEFLGRRVSELEIS-S 59  
Db 1 MSLGIVDAILGKDDRPVKGRVILMKKNVLDFINIGASVVDGISDLLGQKVSQILISGS 60  
Qy 60 VNADPANGLOKRSKAAYLENLWLTNSTPIAAGESAFRTVFDWDDEEFGVPGAFIKNLHF 119  
Db 61 VNYD---GLEGLSNPAYLESWLTDTITPITAGESTFVFDWDRDEFVPGAFIKNLHL 117  
Qy 120 SEFFLKSLTLEDVPHGKHVFCNSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYREN 179  
Db 118 NEFFLKSLTLEDVPNYKIHFCNSWVYPAFRYKSDRIFFANQAYLPSETPQPLRKYREN 177  
Qy 180 ELVTLRGDGTGLEEDRVVDYAYYNDLGDPKQDLSRPVLGGSSEYPYPRRGRTGRKP 239  
Db 178 ELVALRGDGTGLEEDRVVDYACYNDLGEPEKGEYARPILGGSSEYPYPRRGRTGREP 237  
Qy 240 TKTDPNSESRIPLMSLDIYVPRDERFGHIKLSDFLTALKSIVQLLPEFKALFDSTHN 299  
Db 238 TKADPNCESRNPLMSLDIYVPRDERFGHVKKSDFLTSLKSSLTQLTLLPAFKALCDNTPN 297  
Qy 300 EFDSEFDVLKLYEGGIKLPOGPLLKAITDSIPLEILKELLRSDEGLFKYPTPQVIQEDK 359  
Db 298 EENSFADVLNLYEGGIKLPEGPWLKAITDNISSEILKDILQTDGQLLKYPPTQVIQGDK 357  
Qy 360 TAWRTDEEFGREMLAGVNPVILSRLOEFPKSKLDPKIYGNQNSTITREQIEDKLDGLTI 419  
Db 358 TAWRTDEEFGREMLAGSNPVLISRLQEFFPKSKLDPTIYGNQNSTITTEHVQDKLGLTV 417  
Qy 420 DEAIKTNRLFILNHHDLMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPH 479  
Db 418 NEAIKSNRLFILNHHDIVMPLLRKINMSANTKAYASRTLLFLQDDRTLKPLAIELSLPH 477  
Qy 480 DGDQFGAVSKVYTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFFVIATN 539  
Db 478 DGDQFGTVSKVYTPADQGVESIWQFAKAYAVNDMGIHQLISHWLNTHAVIEPFFVIATN 537  
Qy 540 RQLSALHPIYKLLHPHFRETMINALARQILINGGGLLELTVFPAKYSMEMSAVVYKDW 599  
Db 538 RHLVSLHPIHKLLHPHFRTMINALARETLTVDGG-FETSLFPAKYSMEMSAAAYKDW 596  
Qy 600 FPEQALPTDLIKRGVAVEDSSSPLGIRLLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKS 659  
Db 597 FPEQALPADLLKRGVAVEDLSSPHGIRLLILDYPYAVDGLGEIWAIAKSWVTEYCKFFYKS 656  
Qy 660 DDAVQKDTLQAWWKELREEGHGDKKDEPWPWKMTQVQELIDSCCTIITIIWIASALHAAVNF 719  
Db 657 DETVEKDTLQAWWKELREEGHGDKKDEAWWPKLQTRQELRDCCTIITIIWIASALHAAHF 716  
Qy 720 GQYPYAGYLPNRPPTLSRNFMEPEPGSPYEELKTNPDVKFLKTIPTQLOTLGLISLIEILS 779  
Db 717 GLYSYAGYLPNRPPTLSCNLMPEPGSVYEELKTNPDVKFLKTFVPQLQSLLEISIFEVSS 776  
Qy 780 RHSSDTLYLGQRESPEWTKDQPLSAFARFGKKLSLIEDQIMQMNVDKWKNRSGPVKVP 839



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Db 777 RHASDEVYLGORDSIEWTKDKEPLVAFERFGKMLSDIENRIMIMNSHKSWKNRSGPVNVP 836
Qy 840 YTLFPTSEGGLTGKIPNSVSI 862
Db 837 YTLFPTSEGGLTGKIPNSVSI 859

RESULT 15
Q43189 PRELIMINARY; PRT; 861 AA.
ID Q43189;
AC Q43189;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lipoxxygenase (EC 1.13.11.12).
GN Name=POTLX-1;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolomiets M.V., Hannapel D.J., Gladon R.J.;
RT "Potato Lipoxxygenase Genes Expressed During the Early Stages of
RT Tuberization (Accession Nos. U60200 and U60201) (PGR96-065).";
RL Plant Physiol. 112:446-446(1996).
CC -!- FUNCTION: Plant lipoxxygenase may be involved in a number of
CC diverse aspects of plant physiology including growth and
CC development, pest resistance, and senescence or responses to
CC wounding (By similarity).
CC -!- CATALYTIC ACTIVITY: Linoleate + O(2) = (9Z,11E)-(13S)-13-
CC hydroperoxyoctadeca-9,11-dienoate.
CC -!- COFACTOR: Iron (By similarity).
CC -!- SIMILARITY: Belongs to the lipoxxygenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; U60200; AAB67858.1; -.
DR HSSP; P08170; 1FGT.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxxygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000907; Lipoxxygenase.
DR InterPro; IPR001024; Lipoxxygenase_LH2.
DR InterPro; IPR001246; Plant lipoxxygenase.
DR InterPro; IPR008976; PLAT_LH2.
DR Pfam; PF00305; Lipoxxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00468; PLTLPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Dioxygenase; Oxidoreductase.
SQ SEQUENCE 861 AA; 96973 MW; 11AA977F04FF1C56 CRC64;
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Query Match 80.0%; Score 3625.5; DB 2; Length 861;  
Best Local Similarity 78.9%; Pred. No. 4.8e-233;  
Matches 672; Conservative 83; Mismatches 94; Indels 3; Gaps 3;

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Qy 12 GKDDGKKVKGTIVLMKKNVLDFTDINASVLGDVLEFLGRRVSLELISSVNADPANGLOK 71
Db 12 GHDDSKKKVKGTVVMNKNVLDFTDLASSLTCKIFDVLGQKVSFQLISSVQGDPTNGLQK 71
Qy 72 RSKAAYLENWLTNSTPIAAG-ESAFRVTFDWDDEEFGVPGAFIKNLHFSEFFLKSLTLE 130
Db 72 HSNPAYLENSLFTLTPLTAGSETAFGVTFDW-NEEFGVPGAFIKNMHITFEFFLKSLTLE 130
Qy 131 DVPNHGKVHFVNCNSWWYPANKYKSDRIFFANQAYLPSETDTLRKYRENELVTLRGDGTG 190
Db 131 DVPNHGKVHFVNCNSWWYPSLNYSKSDRIFFANQAYLPSETPELLRKYRENELVTLRGDGTG 190
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Qy 191 KLEEWDRVVDYAYYNDLGDPDKGQDLRPPVLGSSSEYYPYRRGRTRGKPTKTDPNSESRI 250
Db 191 KREAWDRYDYDIYNDLGNPDQKENVRTLGGSAEYPYRRGRTRGPTRTDPKSESRI 250
Qy 251 PLLMSLDIYVPRDERFGHIKLSDFLTFAKLSIVQLLLPEFKALFDSTHNEFDSFEDVLKL 310
Db 251 PLILSTDIYVPRDERFGHLKMSDFLTVALKSIVQFILPELHALFDGTPNEFDSFEDVRL 310
Qy 311 YEGGIKLPOGPLLKAITDSIPLEILKELLRSDEGLFKYPTPQVTOEDKTAWRTDEEFG 370
Db 311 YEGGIKLPOGPLFKALTAAPLEIMIRELLRTDGEGLRFPPTPLVINKDSTAWRTDEEFAR 370
Qy 371 EMLAGVNPVSIISRLQEFPPKSKDPKIYGNQNSTITREQIEDKLDGLTIDEAIKTNRLFI 430
Db 371 EMLAGTNPVSIISRLQEFPPKSKLDPEAYGNQNSTITAEHIEDKLDGLTVDEAMNNKLF 430
Qy 431 LNHHDILMPYLRRINTSTDTKTVASRTLLFLQDNGTLKPSAIELSLPHPDGQFGAVSKV 490
Db 431 LNHHDLLIPYLRRINT-TITKTYASRTLLFLQDNGSLKPLAIELSLPHPDGQFGVTSKV 489
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Db 490 YTPSDQGVESIWOLAKAYAVAVNDSGVHQLISHWLNTHAVIEPFVIATNRQLSVLHPIHK 549
Qy 551 LLHPHFRETMINALARQIILINGGGLLELTVPFPAKYSMEMSAVVYKDWVPPEQALPTDLI 610
Db 550 LLYPHFRDTMINALARQILINAAGVFESTVFQSKFALEMSAVVYKDWVPFPDQALPADLV 609
Qy 611 KRGVAVEDSSSPLGIRLLIQDYPAVDGLKIWSAISKSWVTEYCNYYKSDDAVQKDTLQ 670
Db 610 KRGVAVEDSSSPHGVRLLIEDYPYAVDGLIWSAISKSWVTDYCSFYGSDEEILKDNELQ 669
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Db 730 RATVSRRFMPPEPGTPEYEELKKNPKDKAFLKTIPTAQLOTLGLVSLVELSRHTTDEIYLGQ 789
Qy 791 RESPEWTKDQEPLSAFARFGKLSIEDQIMQMNVDKWKNRSGPVKVPYTYLLPPTSEGG 850
Db 790 RESPEWTKDKEPLAAAFDRFGKLTLDIEKQIIQRNGDNILNRSRGPVNAPYTYLLPPTSEGG 849
Qy 851 LTGKGIPNSVSI 862
Db 850 LTGKGIPNSVSI 861
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Search completed: March 10, 2005, 19:02:04  
Job time : 189 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:52:42 ; Search time 45 Seconds  
(without alignments)  
1429.944 Million cell updates/sec

Title: US-10-731-642A-1  
Perfect score: 4534  
Sequence: 1 MFLEKIVDAITGKDDGKKVK.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3610	79.6	859	4	US-09-978-522-3 Sequence 3, Appli
2	3576	78.9	862	4	US-09-978-522-1 Sequence 1, Appli
3	2905	64.1	857	4	US-09-751-687-17 Sequence 17, Appl
4	2779.5	61.3	864	4	US-09-810-268-3 Sequence 3, Appli
5	2745.5	60.6	865	4	US-09-751-687-16 Sequence 16, Appl
6	2680	59.1	862	4	US-09-751-687-9 Sequence 9, Appli
7	2673	59.0	862	4	US-09-751-687-12 Sequence 12, Appl
8	2656	58.6	839	4	US-09-751-687-15 Sequence 15, Appl
9	2584.5	57.0	864	4	US-09-751-687-18 Sequence 18, Appl
10	1746.5	38.5	901	4	US-09-714-767A-4 Sequence 4, Appli
11	558.5	12.3	675	4	US-09-902-540-12713 Sequence 12713, A
12	546	12.0	674	4	US-09-949-016-5980 Sequence 5980, Ap
13	546	12.0	689	4	US-09-949-016-11692 Sequence 11692, A
14	537.5	11.9	677	3	US-09-061-768A-4 Sequence 4, Appli
15	537.5	11.9	677	4	US-09-764-246-4 Sequence 4, Appli
16	537	11.8	711	4	US-09-547-435-2 Sequence 2, Appli
17	537	11.8	867	4	US-09-547-435-24 Sequence 24, Appl
18	527	11.6	556	4	US-09-547-435-6 Sequence 6, Appli
19	510.5	11.3	701	3	US-09-087-727-2 Sequence 2, Appli
20	510.5	11.3	701	4	US-09-853-053-2 Sequence 2, Appli
21	510.5	11.3	701	4	US-09-949-016-6026 Sequence 6026, Ap
22	496	10.9	676	3	US-09-061-768A-2 Sequence 2, Appli
23	496	10.9	676	4	US-09-764-246-2 Sequence 2, Appli
24	496	10.9	676	4	US-09-949-016-6027 Sequence 6027, Ap
25	496	10.9	679	4	US-09-949-016-8912 Sequence 8912, Ap
26	487	10.7	662	3	US-09-061-768A-25 Sequence 25, Appl
27	487	10.7	662	4	US-09-764-246-25 Sequence 25, Appl

28	469.5	10.4	663	4	US-09-641-638-653	Sequence 653, App
29	469.5	10.4	663	4	US-10-170-097-653	Sequence 653, App
30	450.5	9.9	615	4	US-09-547-435-10	Sequence 10, Appl
31	450.5	9.9	771	4	US-09-547-435-28	Sequence 28, Appl
32	441.5	9.7	582	3	US-09-413-814-83	Sequence 83, Appl
33	440.5	9.7	460	4	US-09-547-435-12	Sequence 12, Appl
34	414.5	9.1	692	4	US-09-252-991A-19668	Sequence 19668, A
35	390	8.6	291	4	US-09-547-435-14	Sequence 14, Appl
36	303.5	6.7	195	4	US-09-547-435-20	Sequence 20, Appl
37	266	5.9	489	4	US-09-547-435-4	Sequence 4, Appli
38	266	5.9	645	4	US-09-547-435-26	Sequence 26, Appl
39	256	5.6	334	4	US-09-547-435-8	Sequence 8, Appli
40	172.5	3.8	477	4	US-09-902-540-12721	Sequence 12721, A
41	133.5	2.9	139	4	US-09-547-435-18	Sequence 18, Appl
42	126.5	2.8	1309	4	US-09-975-413A-10	Sequence 10, Appl
43	119	2.6	69	4	US-09-547-435-16	Sequence 16, Appl
44	118.5	2.6	1589	3	US-09-356-952-4	Sequence 4, Appli
45	117.5	2.6	1788	2	US-08-962-284-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-978-522-3  
; Sequence 3, Application US/09978522  
; Patent No. 6787684  
; GENERAL INFORMATION:  
; APPLICANT: Descenzo, Richard  
; APPLICANT: Ireland, Nancy  
; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera  
; FILE REFERENCE: 29520/37890  
; CURRENT APPLICATION NUMBER: US/09/978,522  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 60/241,220  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 859  
; TYPE: PRT  
; ORGANISM: Vitis LOX 2  
US-09-978-522-3

Query Match		79.6%;	Score 3610;	DB 4;	Length 859;
Best Local Similarity		76.9%;	Pred. No. 0;		
Matches		661;	Conservative	106;	Mismatches 91; Indels 2; Gaps 2;
QY	3	LEKIVDAITGKODGKKVGT	VVLMKKNVLDFTDINASVLDGVLEF	GLGRRVLSLELISSVNA	62
Db	2	IHSIVGAITGENDKKIKGT	VVLMKKNVLDNFENASVLDRVHLLGQGVPLQVLSAVHG	61	
QY	63	DPANGLQKRSKAAAYLENWLT	NSTPIAAGESAFRVTFDWDDEEFGVPGAF	IIKNLHFSEF	122
Db	62	DPANGLQKIGKPAYLEDWIT	TITSLTAGESAFKVTFDW-DEEIGEPGAF	IIRNNHSEF	120
QY	123	FLKSLTLEDV	PNHGKVHFCVNSWVYP	PANKYKSDRIFFANQAYLPSET	PDTLRKYRENELV 182
Db	121	YLRTLTLEDV	PGRIHFVNSWVYP	PAQHYKTD	RVFFTNQTYLPSETPGPLRKYREGLV 180
QY	183	TLRGDGTGKLEEDRVYDYAYYNDL	GD	PKQDLSR	PVLGSSSEYPYPRRGRTGRKPTKT 242
Db	181	NLRGDGTGELKEWDRVYDYAYYNDL	GNPDRDLKYAR	PVLGSSAEYPYPRRGRTGRPPSEK	240
QY	243	DPNSESRIPL	MLMSLDIYVPRDER	FGHIKLSDFLT	FALKSIVQLLLPEFKALFDSTHNEFD 302
Db	241	DPNTESRL	PLVMSLNIYVPRDER	FGHLKMSDF	LAYALKSIVQFLLEFEALCDITHNEFD 300
QY	303	SFEDVLKLYEGGI	KLPGQLKAITDSI	PLEILKELLRS	DGEGLFKYPTPQVIOEDKTAW 362
Db	301	SFQDVLDLYEGGI	KVPEGPLLDKIKDNI	PLEMLKELVRTDGEHLFKFPMQV	IKEDKSAW 360
QY	363	RTDEEFGREMLAGNP	VVISRLQEFPPKSKLDPKI	YGNQNS	STITREQIEDKLDGLTIDEA 422



Db 361 RTDEEFAREMLAGLNPVIRLLQEFPPKSKLDPEVYGNQNSSITKEHIENHLDDLTINEA 420  
Qy 423 IKTNRFLFILNHHDIILMPYLRRINTSTDTKTYASRLLFLQDNGTLKPSAIELSLPHPDGD 482  
Db 421 MEKKRFLFILDHHDVFMPLYRRINT-TSTKTYASRLLFLKDDGTLKPLAIELSLPHPSGD 479  
Qy 483 QFGAVSKVYTPADQGVESGIWQAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQL 542  
Db 480 KFGAVNKVYTPAENGVEGSIWQAKAYAAVNDSGYHQLLHSHWLNTHAAIEPFVIATNRQL 539  
Qy 543 SALHPIYKLLHPHFRETMINALARQILINGGGLLELTVFPKYSMEMSAVVYKDWVFP 602  
Db 540 SVLHPIHKLHPHFRTMINALARQILINAGGVVESTVFPKYSMEMSSVVYKDWVLTE 599  
Qy 603 QALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSDDA 662  
Db 600 QALPADLIKRGMAVEDSEAPHGLRLLIDDDYPYAVDGLIWSAIEIETWVKEYCSFYKTD 659  
Qy 663 VQKDTLQAWKELREEGHGDKKDEPWPQKMTVQELIDSCITTIWIASALHAAVNFQY 722  
Db 660 VQKDSLSQSWKKEVREEGHGDKKDEPWPQKMTVKELIETCTIIIWVASALHAAVNFQY 719  
Qy 723 PYAGYLPNRPTLSRNFMPPEGSPPEYELKTNPDKVFLKTTIPQQLTLLGISLIEILSRHS 782  
Db 720 PYAGYLPNRPTISRFRMPEEGTPEYELKSNPDKAFKLTITTAQLTLLGISLIEVLSRHS 779  
Qy 783 SDTLYLGQRESPEWTKDQELPSAFARFGKKLSIEDIQIMQMVNDEKWKNSRGPVKVPYTL 842  
Db 780 SDEVYLGQRTPEWTLDTTPLKAFAKFGKRLADIEMIIDRNGNERFKNRVGPVKIPYTL 839  
Qy 843 LFPTSEGGLTGKIPNSVSI 862  
Db 840 LYPTSEGGLTGKIPNSVSI 859

RESULT 2

US-09-978-522-1  
; Sequence 1, Application US/09978522  
; Patent No. 6787684  
; GENERAL INFORMATION:  
; APPLICANT: Descenzo, Richard  
; APPLICANT: Ireland, Nancy  
; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera  
; FILE REFERENCE: 29520/37890  
; CURRENT APPLICATION NUMBER: US/09/978,522  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 60/241,220  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 862  
; TYPE: PRT  
; ORGANISM: Vitis LOX 1  
US-09-978-522-1

Query Match 78.9%; Score 3576; DB 4; Length 862;  
Best Local Similarity 76.2%; Pred. No. 0;  
Matches 655; Conservative 109; Mismatches 94; Indels 2; Gaps 2;

Qy 3 LEKIVDAITGKDDGKKVKGTIVLMKKNVLDFTDINASVLDGVLEFLGRRVSLLEISSVNA 62  
Db 5 LLSIVSAITGENDKKIEGTIVLMKKNVLDNFNAPVRDRVRHELFGQVSLQVSAVHG 64  
Qy 63 DPANGLOKRSKAAYLENWLTNSTPIAGESAFAFRVTFDWDDEEFGVPGAFIKNLHFSEF 122  
Db 65 DPANGLOKLGKPAYLEDWITITSLTAGESAFKVTFDW-DEEIGFPGAFIIRNNHSEF 123  
Qy 123 FLKSLTLEDVPHGKVHFCVNCNSWVYPANKYKSDRIFFANQAYLPSETPTTLRKYRENELV 182  
Db 124 YLRTLTLLEDVPGRIHFVCNCSWVYPAPKHYKTDVFFFTNTQYLPSETPGPLRKYRKGELV 183

Qy 183 TLRGDTGKLEEDRVVDYAYYNDLGDGDPKQDLSRPLVGLSSSEYPYPRRGRTGRKPTKT 242  
Db 184 NLRGDTGKELKEWDRVDYAYYNDLGPDRDLKYARPLVGLSSAEYPYPRRGRTGRPPSEK 243  
Qy 243 DPNSERIPLLMSLDIYVPRDERFGHIKLSDELTFAKLSIVQLLLPEFKALFDSHNEFD 302  
Db 244 DPKTESRLPLVMSLNIYVPRDERFGHLKMSDFLAYALKSIVQFLLEPEFALCDITPNEFD 303  
Qy 303 SFEDVLKLYEGGIKLPQGPLLKAITDSIPLEILKELLRSDGEGLFKYPTPOVIOEDKTAW 362  
Db 304 SFQDVLDLYEGGIKVPEGPLLDKIKDNIPLLEMLKELVRTDGEHLFKFPMPOVIKEDKSAW 363  
Qy 363 RTDEEFGREMLAGVNPVVISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEA 422  
Db 364 RTDEEFAREMLAGLNPVIRLLQEFPPKSKLDPEVYGNQNSSITKEHIENHLDDLTINEA 423  
Qy 423 IKTNRFLFILNHHDIILMPYLRRINTSTDTKTYASRLLFLQDNGTLKPSAIELSLPHPDGD 482  
Db 424 MEKKRFLFILDHHDVFMPLYRRINT-TSTKTYASRLLFLKDDGTLKPLAIELSLPHPDGD 482  
Qy 483 QFGAVSKVYTPADQGVESGIWQAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQL 542  
Db 483 KFGAVNKVYTPAEDGVEGSIWQAKAYAAVNDSGYHQLLHSHWLNTHAAIEPFVIATNRQL 542  
Qy 543 SALHPIYKLLHPHFRETMINALARQILINGGGLLELTVFPKYSMEMSAVVYKDWVFP 602  
Db 543 SVLHPIHKLHPHFRTMINALARQILINAGGVVESTVFPKYSMEMSSVVYKDWVLTE 602  
Qy 603 QALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSDDA 662  
Db 603 QALPADLIKRGMAVEDSEAPHGLRLLIDDDYPYAVDGLIWSAIEIETWVKEYCSFYKTD 662  
Qy 663 VQKDTLQAWKELREEGHGDKKDEPWPQKMTVQELIDSCITTIWIASALHAAVNFQY 722  
Db 663 VQKDSLSQSWKKEVREEGHGDKKDEPWPQKMTVKELIETCTIIIWVASALHAAVNFQY 722  
Qy 723 PYAGYLPNRPTLSRNFMPPEGSPPEYELKTNPDKVFLKTTIPQQLTLLGISLIEILSRHS 782  
Db 723 PYAGYLPNRPTISRFRMPEEGTPEYELKSNPDKAFKLTITTAQLTLLGISLIEVLSRHS 782  
Qy 783 SDTLYLGQRESPEWTKDQELPSAFARFGKKLSIEDIQIMQMVNDEKWKNSRGPVKVPYTL 842  
Db 783 SDEVYLGQRTPEWTLDTTPLKAFAKFGKRLADIEMIIDRNGNERFKNRVGPVKIPYTL 842  
Qy 843 LFPTSEGGLTGKIPNSVSI 862  
Db 843 LYPTSEGGLTGKIPNSVSI 862

RESULT 3

US-09-751-687-17  
; Sequence 17, Application US/09751687  
; Patent No. 6660915  
; GENERAL INFORMATION:  
; APPLICANT: Douma, Anneke  
; APPLICANT: Doderer, Albert  
; APPLICANT: Cameron-Mills, Verena  
; APPLICANT: Skadhauge, Birgitte  
; APPLICANT: Bech, Lene  
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY  
; FILE REFERENCE: 11225.11US01  
; CURRENT APPLICATION NUMBER: US/09/751,687  
; CURRENT FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 857  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-751-687-17

Query Match 64.1%; Score 2905; DB 4; Length 857;  
Best Local Similarity 63.3%; Pred. No. 1.3e-271;















Db 480 DAFEEYVGGVLRHFYRTDADLEADTEMQQWKKDLTE--HGLPVDKLPCELRRLRRVDDLVDI 537  
Qy 703 CTITIWIASALHAAVNFQYYPAGYLPNRPRTLNRNMP-EPGSPYEELKTNPDKVFELKT 761  
Db 538 LTTVLFTVSVQHAAVNYLQYEHYAFVFNAPLSMRREPFRQKGTIRAEDI---PEMIPTKS 594  
Qy 762 ITPQLQTLGLISLIEILSRHSSDTLYL----GQRESPEWTKDQEPLSAFARFGKKLSDIE 817  
Db 595 -----QMLWQVAIGRALSSFGDDEEYLLHEGGWRE--EYFHEPELVAIRQRFQERLRAOR 647  
Qy 818 DQIMQMNVDKWKNSRGPVKVPYTLLEP 845  
Db 648 EAV-----EARNAGAEVPTYTLRP 666

RESULT 12  
US-09-949-016-5980  
; Sequence 5980, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5980  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-5980

Query Match 12.0%; Score 546; DB 4; Length 674;  
Best Local Similarity 25.0%; Pred. No. 2.4e-43;  
Matches 197; Conservative 119; Mismatches 272; Indels 200; Gaps 27;

Qy 103 DEEFGVPGAFIKNLHF--SEFFLKSLTLEDVPHGKVFHVCNSWVYPANKYKSDRIFF 159  
Db 59 DEELGEIQLVRIEKKRYWLNDWYLYITLK-TPHGDYIEFFCYRWI----- 104  
Qy 160 ANQAYLPSETPDLTKRYRENELVTLRGDTGKLEEDRWVYDYAYNDLGDPKQDLSRP 219  
Db 105 -----TGDV-----EVVLR-DGRAKLARDDOIHLKQHR----- 132  
Qy 220 VLGSSEYPPRRGRTRKPTKTDPN-----ESRIPLMSLDIY--VPRDERFGHIKL 271  
Db 133 -----RKELETRQKQYRWMEWNPGLPLSIDAKCHKDLPRDIOFDSEKG 175  
Qy 272 SDFLTFAKLSIVQLLPEFKALFDSHTNEFDSFEDVLKLYEGGIKLPQGPLLKAITDSIP 331  
Db 176 VDFVLNYSKAMENLFINRFMHMFQSSWNDFADFEKIF-----VK-----ISNTIS 220  
Qy 332 LEILKELRSDEGLFKYPTPQVIQEDKTAWRTDEEFGREMLAGVNPVIISRLQEFPPKS 391  
Db 221 ERVMNH-----WQEDLMFGYQFLNGCNFVLIRRCTELPEK- 255  
Qy 392 KLDPKIYGNQNSTITREQIEDKLD-GLTIDEAIKTNRLFILNHHIDILMPYLRRINTSTDT 450  
Db 256 -----LPVTTEMVECSLERQLSLEQEVQGNIFIVDFE--LLDGIDANKTDPCT 302  
Qy 451 KTYASRTLLFLQDNGTLKPSAIELSLPHPDGDQFGAVSKVYTPADQGVESIWQLAKAYA 510  
Db 303 LQFLAAPICLLYKNLANKIVPIAIQLNQIPGDE----NPIFLPSDAKYD---WLLAKIWT 355

Qy 511 AVNDSGVHQLISHWLNTHAAIEPFVIATNRQLSALHPIYKLLPHPHFRETMINALARQIL 570  
Db 356 RSSDFHVHTITHLLRTHLVSEVFGIAMYRQLPAVHPFKLLVAHVFTIAINTKAREQL 415  
Qy 571 I-----NGGGLLELTVFPKYSMEMSAVVVKDWVFPPEQALPTDLIKRGVAVED 618  
Db 416 ICEGGLFDKANATGGGGHVQMV-----GRAMKDLTVASLCFPEA-----IKARGMESKE 464  
Qy 619 SSSPLGIRLLLIQDYPYAVDGLKIWSAISKSWTTEYCNYYKSDDDAVQKDTTELQAWWKELRE 678  
Db 465 D-----IPYFYRDDGLLVWEAIRTFTAEVVDIYEGDQVVEEDPELQDFVNDVVV 515  
Qy 679 ECHGDKKDEPWPMQTVQELIDSCITITIWIASALHAAVNFQYYPAGYLPNRPITLSRNF 738  
Db 516 YGMRGRKSSGFPKSVKSRQLSEYLTVVIFTASQAQAAVNFQYDWCWIPNAPTMR-- 573  
Qy 739 MPEP---GSPEYEELKTNPDKVELKTTITPQLQTLGLISLIEILSRHSSDTLYLGQRESPE 795  
Db 574 APPPTAKGVVTIEQI-----VDTLPDRGRSCHWHLGAVWALSQFOENELFLGM--YPE 623  
Qy 796 WTKDQEP-L-SAFARFGKKLSDIEDQIMQMNVDKWKNSRGPVKVPYTLTLLFPTSEGGLTGK 854  
Db 624 EHFIKPVKEAMARFRKNLEAIVSIAERNKKK-----QLPYYLSPDR----- 667  
Qy 855 GIPNSVSI 862  
Db 668 -IPNSVAI 674

RESULT 13  
US-09-949-016-11692  
; Sequence 11692, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11692  
; LENGTH: 689  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11692

Query Match 12.0%; Score 546; DB 4; Length 689;  
Best Local Similarity 25.0%; Pred. No. 2.5e-43;  
Matches 197; Conservative 119; Mismatches 272; Indels 200; Gaps 27;

Qy 103 DEEFGVPGAFIKNLHF--SEFFLKSLTLEDVPHGKVFHVCNSWVYPANKYKSDRIFF 159  
Db 74 DEELGEIQLVRIEKKRYWLNDWYLYITLK-TPHGDYIEFFCYRWI----- 119  
Qy 160 ANQAYLPSETPDLTKRYRENELVTLRGDTGKLEEDRWVYDYAYNDLGDPKQDLSRP 219  
Db 120 -----TGDV-----EVVLR-DGRAKLARDDOIHLKQHR----- 147  
Qy 220 VLGSSEYPPRRGRTRKPTKTDPN-----ESRIPLMSLDIY--VPRDERFGHIKL 271  
Db 148 -----RKELETRQKQYRWMEWNPGLPLSIDAKCHKDLPRDIOFDSEKG 190  
Qy 272 SDFLTFAKLSIVQLLPEFKALFDSHTNEFDSFEDVLKLYEGGIKLPQGPLLKAITDSIP 331  
Db 191 VDFVLNYSKAMENLFINRFMHMFQSSWNDFADFEKIF-----VK-----ISNTIS 235



RESULT 15

US-09-764-246-4  
; Sequence 4, Application US/09764246  
; Patent No. 6649355  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; BOEGLIN, WILLIAM E.  
; JISAKA, MITSUO

TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/764,246  
FILING DATE: 17-Jan-2001  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 677 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-764-246-4

Query Match 11.9%; Score 537.5; DB 4; Length 677;  
Best Local Similarity 25.6%; Pred. No. 1.6e-42;  
Matches 205; Conservative 110; Mismatches 290; Indels 195; Gaps 30;

Qy	89	AAGESAFRVTFDWD-----DEFGVPGAFIIKNLHFSEFFLKSLTLEDVFNHG	136
Db	47	AGAEEDFEVTLPQDVGTVLMRLRVHKAPVSLP----LMSFRSDAWFCRWFELEWLPG-A	101
Qy	137	KVHFVCNSWVYPANK--YKSDRIFFANQAYLPSETPTDLRKRYRENELVTLRGDGTGK--L	192
Db	102	ALHFPCYQWLEGAGELVLRREGAAKVSQDHP-----TLQDQRQKELESRQKMYSWKTYI	156
Qy	193	EEWDRVYDYAYNDLGDGPKQDLRSPVLGSGSEYPYPRRGRTGKPKTKTDPNSESRIPL	252
Db	157	EGWPRCLDHETVKDL-----DL-----	173
Qy	253	LMSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLLPEFKALFDSITHNEFDSFEDVLKLYE	312
Db	174	-----NIKYS-----AMKN-----AKLFFKAHSAYTELK-----	197
Qy	313	GGIKLPQGPLLKAITDSIPL-EILKELRSDGCEGLFKYPTPQVIOEDKTAWRTDEEFGRE	371
Db	198	-----VKGLLDRGTGLWRSLEMR-----LFNFRKTPAAEYVFAHWQEDAFFASQ	242
Qy	372	MLAGVNPVIISRLQEPFPPKSKLDPKIYGNQNSTITREQIEDKL-DGLTIDEAIAKTNRLFI	430

Db	243	FLNGINPVLIIRCHSLP-----NNFPVTDEMVPVLGPGTSLQAELEKGSFL	290
Qy	431	LNHHDILMPYLRRINTSTDTKYASRTLFLQD-NGTLKPSAIEL-SLPHPDGDQFGAVS	488
Db	291	VD-HGILSGVHTNILNGKPQFSAAPMTLLHQSSGSGPLLPJAIQLKQTPGPD-----N	342
Qy	489	KVYTPADQGVESIMQAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQLSALHPI	548
Db	343	PIFLPSDDTDW---WLLAKTWVRNSEFYIHEAVTHLLHAHLIPEVFALATLRQLPRCHPL	399
Qy	549	YKLLHPHFRETMINALARQILINGGGLLELTV-----FPAKYSMEMSAVVYKDWVPEE	602
Db	400	FKLLIPHIRYTLHINTLARELLVAPGKLIDKSTGLGTGGSFSDLIKRNMEQLNYS-----V	454
Qy	603	QALPTDLIKRGVAVEDSSSPGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYYKSDDA	662
Db	455	LCLPEDIRARG--VED-----IPGYVYRDDGMQIWAISFVSEIVSIYYPSTDS	502
Qy	663	VQKDTLQAWKELREEGHGDKKDEPWWPKMQTVQELIDSCITITIWIASALHAAVNFQY	722
Db	503	VQDDQELQAWREIFSEGLGRESSGMPSLDRTREALVQYITMVIFTCSAKHAAVSSQGF	562
Qy	723	PYAGYLPNRPTLSRNFMPPEPGSPYEELKTNPKVFLKTIPTPOLQTLGSLIEILSRHS	782
Db	563	DSCVWMPNLPPTMQ--LPPPTS---KGQARPES-FIATLPAVNSSSYHIIALWLLSABP	615
Qy	783	SDTLYLGQRESPEWTKDQELSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPVKVPYTL	842
Db	616	GQORPLGHYPDEHFTED-APRRSVAAFQKLIQISKGI-----RERNRGLALPTY	665
Qy	843	LFPTSEGGLTGKIPNSVSI	862.
Db	666	LDPPL-----IENSVSI	677

Search completed: March 10, 2005, 19:03:44  
Job time : 50 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 13, 2005, 23:06:59 ; Search time 9293 Seconds  
(without alignments)  
4494.608 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database :

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ACCESSION	X84040.1 GI:899343					
VERSION	lipoxxygenase; Lox1 gene.					
KEYWORDS	Nicotiana tabacum (common tobacco)					
SOURCE	Nicotiana tabacum					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.					
REFERENCE	1					
AUTHORS	Veronesi,C., Fournier,J., Rickauer,M., Marolda,M. and Esquerre-Tugaye,M.T.					
TITLE	Nucleotide sequence of an elicitor-induced tobacco lipoxxygenase cDNA (PGR95-009)					
JOURNAL	Plant Physiol. 108, 1342-1342 (1995)					
REFERENCE	2 (bases 1 to 2888)					
AUTHORS	Esquerre-Tugaye,M.T.					
TITLE	Direct Submission					
JOURNAL	Submitted (24-JAN-1995) M.T. Esquerre-Tugaye, Universite Paul Sabatier, URA 1941 CNRS, Centre de Biologie et Physiol. Vegetales, 118 route de Narbonne, 31062 Toulouse, FRANCE					
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4534	100.0	3390	6 AX644612	AX644612 Sequence
3	4095	90.3	2915	8 AY008278	AY008278 Lycopersi
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DEFINITION Sequence 2 from Patent WO02099112.

ACCESSION AX644612

VERSION AX644612.1 GI:28610627

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Mene-Saffrane,L., Esquerre-Tugaye,M.T., Fournier,J., Beffa,R. and Grosjean-Cournoyer,M.C.

TITLE Lipoxigenase overexpression in plants and reduction in plant sensitivity to diseases and attacks from pathogenic organisms

JOURNAL Patent: WO 02099112-A 2 12-DEC-2002;

FEATURES

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Query Match: 100.00% Indels: 0

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Qy 601 ProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSer 620

Db 2343 CCTGAACAAGCACCTTCCTACTGATCTCATCAAAAGAGGAGTAGTGTGAGGACTCGAGC 2402

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Db 2403 TCCCCACTTGGCATTCGATTACTGATTGAGGACTATCCATATGCTGTGTTGATGGGTTGAAA 2462

Qy 641 IleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAsp 660

Db 2463 ATTTGGTCAGCAATTAAAGTTGGGTAACTGAATACTGCAACTACTATTACAAATCAGAT 2522

Qy 661 AspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGly 680

Db 2523 GATGCGGTTCAAAAAGACACTGAACCTCCAAGCCTGGTGGAAAGAACTCCGCGAAGAGGGA 2582

Qy 681 HisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIle 700

Db 2583 CACGSGTGAACAAGAAAGATGAGCCTTGGTGGCCTTAAATGCAGACAGTGCAGAAGAAATTGATA 2642

Qy 701 AspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGly 720

Db 2643 GACTCTTGACCATCACAAATATGGATAGCTTCAGCACTTCATGCGAGCAGTCAATTTCCGG 2702

Qy 721 GlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetPro 740

Db 2703 CAATACCTTTATGCTGGTTATCTCCCTAATCGCCCTACATTAAAGCCGAAATTTTCATGCCA 2762

Qy 741 GluProGlySerProGluTyrGluLeuLysThrAsnProAspLysValPheLeuLys 760

Db 2763 GAGCCAGGAAGTCCTGAGTATGAAGAGCTCAAGACAAATCCGGATAAGGTATTCTCTCAAA 2822

QY 761 ThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArg 780  
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QY 781 HisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyrThrLysAspGln 800  
Db 2883 CATCTTCGGATACACTTTACCTCGGCAAGGAATCACCTGAATGCAAGGATCAA 2942

QY 801 GluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIle 820  
Db 2943 GAACCACTTTCAGCTTTTGGAGGTTTGGAAAGAGCTGAGTGATATCGAGGATCAGATT 3002

QY 821 MetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProValLysValProTyr 840  
Db 3003 ATGCAGATGAATGTCGATGAGAAATGGAAGAACAGGTCGGTCTCTGTAAAGTTCCATAC 3062

QY 841 ThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerVal 860  
Db 3063 ACCTTGCTCTCCCCACAAGTGAAGGAGGACTTACTGGCAAGGAATTCCTAAACAGTGTG 3122

QY 861 SerIle 862  
Db 3123 TCAATA 3128

RESULT 3  
AY008278  
LOCUS AY008278 2915 bp mRNA linear PLN 11-OCT-2000  
DEFINITION Lycopersicon esculentum lipoxigenase mRNA, complete cds.  
ACCESSION AY008278  
VERSION AY008278.1 GI:10764844  
KEYWORDS  
SOURCE  
ORGANISM  
Lycopersicon esculentum (tomato)  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 2915)  
Pan, Z., Feng, Q., Gilchrist, D.G. and Bostock, R.M.  
Cloning and characterization of a toxin-induced lipoxigenase gene  
in tomato  
Unpublished  
2 (bases 1 to 2915)  
Pan, Z., Feng, Q., Gilchrist, D.G. and Bostock, R.M.  
Direct Submission  
Submitted (20-SEP-2000) Plant Pathology, University of California,  
One Shields Ave., Davis, CA 95616, USA  
Location/Qualifiers  
1. .2915  
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Pred. No.: 0 Length: 2915  
Score: 4095.00 Matches: 762  
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Best Local Similarity: 88.30% Mismatches: 44  
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DB: 8 Gaps: 2

US-10-731-642A-1 (1-862) x AY008278 (1-2915)

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QY 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40  
Db 104 GGAACAGTTGTGTTAATGAAAAAAATGTTTGGATTTTACTGATGTAACCTCAATT 163

QY 41 LeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuIleSerSerVal 60  
Db 164 GTCGATGCTGCTCTTGAATTCTTCGAGAGAGATTCTTTTCAGTTAATCAGTAAT--- 220

QY 61 AsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsn 80  
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QY 81 TrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAsp 100  
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QY 121 GluPheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPhe 140  
Db 401 GAATTCTTTCTCAAGTCACTCACACTTGAACATGTCCTTAATCATGGAAGTCCATTTT 460

QY 141 ValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAla 160  
Db 461 GTATGCAATTCTTGGGTGATCCTGCTTCTAAATACAAGTCTGACCGCATTTTCTTCGG 520

QY 161 AsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGlu 180  
Db 521 AATCAGCTTATCTCCCAAGTGAACACACCAAGATTGTTACGAAAAATACAGAGAAAATGAA 580

QY 181 LeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArgValTyrAsp 200  
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QY 201 TyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProVal 220  
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Db 701 CTTGGAGGATCATCTCAGTATCCGTATCCTCGTAGAGGAGGACAGGACGCAACCAACC 760

QY 241 LysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrVal 260  
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QY 261 ProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLys 280  
Db 821 CCAAGGACGAGCGATTGGACATGTGAAGATGTGAGACTTCTTGACATTTGCTTTTGAAA 880

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Qy 481 GlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGly 500  
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Qy 601 ProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSer 620  
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Qy 621 SerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLys 640  
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Qy 701 AspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaValAsnPheGly 720  
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Qy 860 ValSerIle 862  
Db 2621 GTGCTATA 2629  
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STU60202  
LOCUS Solanum tuberosum lipoxxygenase (POTLX-3) mRNA linear PLN 28-AUG-1997  
DEFINITION Solanum tuberosum lipoxxygenase (POTLX-3) mRNA, complete cds.  
ACCESSION U60202  
VERSION U60202.1 GI:1407704  
KEYWORDS  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiids; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 2831)  
AUTHORS Kolomiets,M.V., Hannapel,D.J. and Gladon,R.J.  
TITLE Nucleotide Sequence of a cDNA Clone for a Lipoxxygenase from  
Abscisic Acid-Treated Potato Leaves (Accession No.  
U60202) (PCR96-069)  
JOURNAL Plant Physiol. 112, 446 (1996)  
REFERENCE 2 (bases 1 to 2831)  
AUTHORS Kolomiets,M.V. and Hannapel,D.J.  
TITLE Direct Submission  
JOURNAL Submitted (07-JUN-1996) Horticulture, Iowa State University, Ames,  
IA 50011, USA  
FEATURES  
source location/Qualifiers  
1 .2831  
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Percent Similarity:	92.48%	Conservative: 64
Best local Similarity:	85.07%	Mismatches: 61
Query Match:	86.77%	Indels: 4
DB:	8	Gaps: 3
US-10-731-642A-1 (1-862) x STU60202 (1-2831)		
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Qy	19 ValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAla	38
Db	99 GTGAAAGGAACAATGTGTGATGAAGAAGATGTACTGGACTTTAATGATGTCATGCC	158
Qy	39 SerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSer	58
Db	159 TCTCTTCTTGAGGAGTACTTGAGTTCCTTGGGAAAGAGTCTCTTTGCAGTTGATCAGC	218
Qy	59 SerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeu	78
Db	219 GTTGTTTCATGCTGATCCTGGAAACAGTTTACAAGGGAAACGTAGCAATCCAGCTTACTT	278
Qy	79 GluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThr	98
Db	279 GAGAAAGTGGCTCACTACAGGAACCTCATTTAGTAGCAGGTGAATCAGCCTTGACGTCAC	338
Qy	99 pheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHis	118
Db	339 TTTTGATTGG--GACGAAGATATTGGCGGTACCAGGGGCAATTTATATCAACAATTTCC	395
Qy	119 PheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysVal	138
Db	396 TTCAATGAGTTTATCTCAAGTCACTCACCTTGAAGATGTTTCCTTAATCATCGCAACGTT	455
Qy	139 HisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhe	158
Db	456 CATTTTGTGCAATTCTTGGGTTTATCTGCTAAAAAATACAAATCAGAACGCATTTTC	515
Qy	159 PheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGlu	178
Db	516 TTTTGCTAATCAGGCATATCTTCCCGGTGAAACACAGAACCAATTCGCAATTACAGAGAA	575

Qy	179 AsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluTrpAspArgVal	198
Db	576 AAAGAATTAGTGAACTTGAGAGGAAATGGAATGGAAGCTTGAGGAATGGGACAGATT	635
Qy	199 TyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArg	218
Db	636 TATGACTACGCATTATACAATGACTTGGGTGATCCAGAAAAAGGCAACAGTATGCCAGG	695
Qy	219 ProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLys	238
Db	696 ACTATCCTCGGAGGATCTGCTGAGTACCCGTACCTCGGAGAGGAAGAACTGGCAGAAAG	755
Qy	239 ProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIle	258
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Qy	259 TyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAla	278
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Db	876 TTGAAATCCATTGTTCAAGTTTCAAGCTTCTTTGATAGCACACCT	935
Qy	299 AsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeuPro	318
Db	936 GATGAGTTTGACAGCTTTGAGGATGTTACTGAAACTTTATGAAGGAGGAATCAAATTGCC	995
Qy	319 GlnGlyProLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeu	338
Db	996 CAAGGCCCTTTTCTTAAAGCCCTCACTGATAGTATTCTCTCTAGAGATTCTAAAAGAAATT	1055
Qy	339 LeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAsp	358
Db	1056 ATCCGAACCGATGGTGAAGGAAAATTCAAATTCCTCAACACCTCAAGTTATTCAAGAGGAT	1115
Qy	359 LysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnPro	378
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Qy	379 ValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyr	398
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Qy	399 GlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThr	418
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Db	1296 ATCGATGATGCAATCAAGACTAACAGGCTTTATATATACTAAACCAACCATGACATCCTTATG	1355
Qy	439 ProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeu	458
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AUTHORS	Geerts,A., Feltkamp,D. and Rosahl,S.		
TITLE	Expression of lipoxxygenase in wounded tubers of Solanum tuberosum L		
JOURNAL	Plant Physiol. 105 (1), 269-277 (1994)		
MEDLINE	94302170		
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US-10-731-642A-1 (1-862) x S73865 (1-2718)			
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Qy	50	ArgArgValSerLeuGluLeuIleSerSerValAsnAlaAspProAlaAsnGlyLeuGln	69
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Qy	70	GlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeuThrAsnSerThrProIleAla	89

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Query Match: 81.34% Indels: 2  
DB: 8 Gaps: 2
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US-10-731-642A-1 (1-862) x LEU09026 (1-2842)

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RESULT 11

STLIPOXT8

LOCUS STLIPOXT8 2808 bp mRNA linear PLN 27-SEP-1996

DEFINITION S.tuberosum mRNA for lipoxxygenase (clone T8).

ACCESSION X95513

VERSION X95513.1 GI:1495815

KEYWORDS lipoxxygenase.

SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

1

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

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AUTHORS

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FEATURES

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polya\_site

2808

ORIGIN

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Best Local Similarity: 79.23% Mismatches: 92

Query Match: 80.36% Indels: 3

DB: 8 Gaps: 3

US-10-731-642A-1 (1-862) x STLIPOXT8 (1-2808)

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asterids; lamiids; Solanales; Solanaceae; Solanum.

REFERENCE 1  
AUTHORS Hughes, R.K., West, S.I., Hornostaj, A.R., Lawson, D.M.,  
Fairhurst, S.A., Sanchez, R.O., Hough, P., Robinson, B.H. and Casey, R.  
TITLE Probing a novel potato lipoxxygenase with dual positional  
specificity reveals primary determinants of substrate binding and  
requirements for a surface hydrophobic loop and has implications  
for the role of lipoxxygenases in tubers

JOURNAL Biochem. J. 353 (Pt 2), 345-355 (2001)  
MEDLINE 21066065  
PUBMED 11139400  
REFERENCE 2 (bases 1 to 2818)  
AUTHORS Casey, R.  
TITLE Direct Submission  
JOURNAL Submitted (15-DEC-1998) R. Casey, John Innes Institute, Colney  
Lane, Norwich NR4 7UH, UK  
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AUTHORS Fidansef,A.L. and Bostock,R.M.			
TITLE Solanum tuberosum (Lehmi Russet) lipoxxygenase (plox2) mRNA,			
complete cds			
JOURNAL Unpublished			
REFERENCE 2 (bases 1 to 2818)			
AUTHORS Fidansef,A.L. and Bostock,R.M.			
TITLE Direct Submission			
JOURNAL Submitted (14-AUG-1997) Plant Pathology Department, University of			
California, Davis, One Shields Avenue, Davis, CA 95616, USA			
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RESULT 14

AF039651

LOCUS AF039651 2843 bp mRNA linear PLN 13-JAN-1999

DEFINITION Solanum tuberosum 5-lipoxygenase mRNA, complete cds.

ACCESSION AF039651

VERSION AF039651.1 GI:2789651

KEYWORDS

SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 2843)

Chen,X., Reddanna,P., Reddy,G.R., Kidd,R., Hildenbrandt,G. and Reddy,C.C.

Expression, purification, and characterization of a recombinant 5-lipoxygenase from potato tuber

Biochem. Biophys. Res. Commun. 243 (2), 438-443 (1998)

98153783

9480827

2 (bases 1 to 2843)

Chen,X., Reddanna,P., Reddy,G.R., Kidd,R., Hildenbrandt,G. and Reddy,C.C.

Direct Submission

Submitted (22-DEC-1997) Veterinary Science, Pennsylvania State University, 226 Fenske, University Park, PA 16802, USA

Location/Qualifiers

1. .2843

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ORIGIN

Alignment Scores:

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Score: 3633.50 Matches: 674

Percent Similarity: 88.85% Conservative: 83

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Query Match: 80.14% Indels: 3

DB: 8 Gaps: 3

US-10-731-642A-1 (1-862) x AF039651 (1-2843)

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QY 52 ValSerLeuGluLeuIleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLys 71

Db 192 GTTCTTTTCAATTAATAGCTCTGTCAAGGTGATCCTACAAATGGTTTACAAGGGAAG 251

QY 72 ArgSerLysAlaAlaTyrLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGly 91

Db 252 CACAGCAATCCAGCCTACTTGGAGAACTCTCTCTTTACTCTAACACCATTAACAGCAGT 311

QY 92 ---GluSerAlaPheArgValThrPheAspTrpAspAspGluPheGlyValProGly 110





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RESULT 15

STLOX1  
LOCUS STLOX1 2809 bp mRNA linear PLN 03-JUL-1995  
DEFINITION S.tuberosum (Desiree) mRNA for lipoxxygenase.  
ACCESSION X79107

VERSION X79107.1 GI:486618

KEYWORDS lipoxxygenase.

SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE 1

AUTHORS Casey, R.  
TITLE Sequence of a cDNA clone encoding a potato (Solanum tuberosum) tuber lipoxxygenase

JOURNAL Plant Physiol. 107 (1), 265-266 (1995)

MEDLINE 95175602

PUBMED 7870815

REFERENCE 2 (bases 1 to 2809)

AUTHORS Casey, R.

TITLE Direct Submission

JOURNAL Submitted (09-MAY-1994) R. Casey, John Innes Institute, Colney Lane, Norwich NR4 7UH, UK

FEATURES

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ORIGIN

Alignment Scores:

Pred. No.: 1.66e-282 Length: 2809  
Score: 3632.50 Matches: 672  
Percent Similarity: 88.62% Conservative: 83  
Best Local Similarity: 78.87% Mismatches: 94

Query Match: 80.12% Indels: 3  
DB: 8 Gaps: 3  
US-10-731-642A-1 (1-862) x STLOX1 (1-2809)  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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4493.979 Million cell updates/sec

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3346.5	73.8	2744	17	US-10-425-114-12761	Sequence 12761, A
3	3254.5	71.8	4237	10	US-09-978-522-4	Sequence 4, Appli
4	3202.5	70.6	2580	9	US-09-938-842A-1504	Sequence 1504, Ap
5	3202.5	70.6	2580	11	US-09-938-842A-1504	Sequence 1504, Ap
6	3138	69.2	4687	10	US-09-978-522-2	Sequence 2, Appli
7	3104.5	68.5	2828	17	US-10-425-114-11204	Sequence 11204, A
8	3087.5	68.1	2867	17	US-10-424-599-70317	Sequence 70317, A
9	3022.5	66.7	2929	14	US-10-059-909-11	Sequence 11, Appli
10	2909	64.2	2782	17	US-10-425-114-7612	Sequence 7612, Ap
11	2909	64.2	2804	17	US-10-425-114-9323	Sequence 9323, Ap
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13	2909	64.2	2940	17	US-10-424-599-73134	Sequence 73134, A
14	2849.5	62.8	2704	17	US-10-425-114-8087	Sequence 8087, Ap
15	2849.5	62.8	2793	17	US-10-424-599-73131	Sequence 73131, A
16	2791.5	61.6	2970	18	US-10-437-963-62749	Sequence 62749, A
17	2783	61.4	2962	17	US-10-424-599-77374	Sequence 77374, A
18	2769.5	61.1	2595	16	US-10-132-350-11	Sequence 11, Appli
19	2769.5	61.1	3007	16	US-10-132-350-9	Sequence 9, Appli
20	2763.5	61.0	2929	17	US-10-425-114-11279	Sequence 11279, A
21	2756.5	60.8	3303	18	US-10-425-115-1821	Sequence 1821, Ap
22	2755.5	60.8	3307	17	US-10-424-599-116102	Sequence 116102,
23	2754	60.7	3037	17	US-10-424-599-96731	Sequence 96731, A
24	2734.5	60.3	2664	16	US-10-132-350-19	Sequence 19, Appli
25	2734.5	60.3	3080	16	US-10-132-350-17	Sequence 17, Appli
26	2733.5	60.3	3003	17	US-10-425-114-34535	Sequence 34535, A
27	2732.5	60.3	2558	17	US-10-425-114-8593	Sequence 8593, Ap
28	2730.5	60.2	2601	18	US-10-437-963-13610	Sequence 13610, A
29	2724.5	60.1	2664	16	US-10-132-350-23	Sequence 23, Appli
30	2724.5	60.1	2664	16	US-10-132-350-27	Sequence 27, Appli
31	2724.5	60.1	3122	16	US-10-132-350-21	Sequence 21, Appli
32	2724.5	60.1	3134	14	US-10-059-909-15	Sequence 15, Appli
33	2704	59.6	2816	17	US-10-425-114-7942	Sequence 7942, Ap
34	2704	59.6	2926	17	US-10-425-114-29333	Sequence 29333, A
35	2704	59.6	3182	18	US-10-437-963-39412	Sequence 39412, A
36	2700.5	59.6	2622	16	US-10-132-350-3	Sequence 3, Appli
37	2700.5	59.6	2874	17	US-10-425-114-17199	Sequence 17199, A
38	2700.5	59.6	2912	16	US-10-132-350-1	Sequence 1, Appli
39	2700.5	59.6	3050	18	US-10-425-115-158034	Sequence 158034,
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42	2694.5	59.4	2744	17	US-10-425-114-7363	Sequence 7363, Ap
43	2694.5	59.4	2755	17	US-10-425-114-11264	Sequence 11264, A
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ALIGNMENTS

RESULT 1  
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; Sequence 2, Application US/10731642A  
; Publication No. US20040205842A1  
; GENERAL INFORMATION:  
; APPLICANT: MENE-SAFFRANE, Laurent  
; APPLICANT: ESQUERRE-TUGAYE, Marie-Therese  
; APPLICANT: FOURNIER, Joelle  
; APPLICANT: BEFFA, Roland  
; APPLICANT: GROSJEAN-COURNOYER Marie-Claire  
; TITLE OF INVENTION: LIPOXYGENASE OVEREXPRESSION IN PLANTS  
; TITLE OF INVENTION: AND REDUCTION IN PLANT SENSITIVITY TO  
; TITLE OF INVENTION: DISEASES AND TO ATTACKS FROM PATHOGENIC  
; TITLE OF INVENTION: ORGANISMS  
; FILE REFERENCE: A36097-PCT-USA-A 075188.0117  
; CURRENT APPLICATION NUMBER: US/10/731,642A  
; CURRENT FILING DATE: 2003-12-08  
; PRIOR APPLICATION NUMBER: PCT/FR02/01943  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: FR 01/07470



;; PRIOR FILING DATE: 2001-06-07  
;; PRIOR APPLICATION NUMBER: FR 01/14358  
;; PRIOR FILING DATE: 2001-11-07  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: Custom  
;; SEQ ID NO 2  
;; LENGTH: 3390  
;; TYPE: DNA  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: construct CamV 35S-LOX  
;; FEATURE:  
;; NAME/KEY: promoter  
;; LOCATION: (1)..(532)  
;; OTHER INFORMATION: CamV 35S promoter  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (543)..(3131)  
;; OTHER INFORMATION: Tobacco LOX1 coding sequence  
;; FEATURE:  
;; NAME/KEY: terminator  
;; LOCATION: (3138)..(3390)  
;; OTHER INFORMATION: Nos terminator  
US-10-731-642A-2

Alignment Scores:  
Pred. No.: 0 Length: 3390  
Score: 4534.00 Matches: 862  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 18 Gaps: 0

US-10-731-642A-1 (1-862) x US-10-731-642A-2 (1-3390)

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QY 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40  
DB 603 GGAACAGTGGTTTTGATGAAGAAAAATGTTTGGATTTTACTGATTAATGCTCAGTT 662  
QY 41 LeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluIleSerSerVal 60  
DB 663 CTTGATGGAGTCTTGAGTTCCTTGGTCGAGGGTCTCTCTCGAGTTGATCAGTTCTGTT 722  
QY 61 AsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsn 80  
DB 723 AATGCTGATCTGCAATGGTTTACAGGGAACGCAGCAAGCAGCATATTTGGAGAAC 782  
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QY 101 TrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSer 120  
DB 843 TGGGATGATGAGGAATTTGGAGTTCAGGAGCATTCATTATCAAGAACTTGCAATTTTAGT 902  
QY 121 GluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPhe 140  
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QY 141 ValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAla 160  
DB 963 GTCTGTAATCTTGGGTTTATCCTGCTAATAAATAATAAGTCAGATCGCATCTTCTTCGCG 1022  
QY 161 AsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGlu 180  
DB 1023 AATCAGGCTTATCTACCAAGTGAAACACCAGACACATTCGGAATAATACAGAGAAATGAA 1082  
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QY 201 TyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProVal 220  
DB 1143 TATGCTTACTACAATGACTTGGGTGATCCAGACAAGGCCAAGATTGTCAAGGCCTGTC 1202  
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QY 281 SerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGlu 300  
DB 1383 TCCATTGTGCAGTTGCTTCTCCCTGAGTTTAAAGGCTTTTGTTCGATAGCACGCATAATGAG 1442  
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QY 401 GlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAsp 420  
DB 1743 CAAAACAGTACAATTACCAGAGAGCAGATAGAGGATAAGTTGGATGGACTAACAATTGAT 1802  
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DB 1803 GAGGCAATCAAGACTAACAGACTATTATATTGAACCATCATGATATCCTTATGCCATAC 1862  
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QY 461 LeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAsp 480  
DB 1923 TTGCAAGATAATGGAACCTTTGAAGCCCATCAGCAATTGAACCTTAAGCTTGCCACATCCAGAC 1982  
QY 481 GlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGly 500  
DB 1983 GGAGATCAATTTGGCGCTGTAGCAAAAGTATATACACCAGCTGATCAAGGTGTTGAAGGT 2042  
QY 501 SerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeu 520  
DB 2043 TCTATCTGGCAGTTGGCCAAAGCCTATGCAGCAGTGAATGATTCGGCGGTTTCATCAACTC 2102  
QY 521 IleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArg 540  
DB 2103 ATCAGTCACTGGTTGAATACATACATGCAGCGATAGAGCCATTCTGTATCGCAACAAATAGG 2162  
QY 541 GlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMet 560  
DB 2163 CAACTAAGCGCGCTTCACCCCTATTATAAGCTTCTCCACCCTCATTTCCGTGAGACGATG 2222



Db 723 CCACAACATGCTCGTCTACTCTAGGAGGGTCTAAGGATTACCCCTACCCCTCGTAGGGGA 782

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Db 843 TCGAGCTTAGACATCTATGTTCCAAGGGATGAAAGATTTGGTCACTTGAAAAATGGCGGAT 902

Qy 274 PheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeu 293

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Qy 294 PheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGly 313

Db 963 TTCGACAGCACCCCTAATGAGTTTGACAAATTTGAAGATGTACTTAAACTCTATGAAGGT 1022

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Db 1080 ATGCTTAAGGAATTTCCGATCTGACGGGCAAGGCTTCTCAAAATTCGGTGCCTCAA 1139

Qy 354 ValIleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeu 373

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Qy 374 AlaGlyValAsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeu 393

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Db 1857 CTTTACAAGGACTGGGTTTTCCCTGAGCAGGCACCTGCCTGAAGACCTTGTCAAGAGAGGA 1916

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RESULT 3

US-09-978-522-4

; Sequence 4, Application US/09978522

; Publication No. US20030033627A1

; GENERAL INFORMATION:

; APPLICANT: Descenzo, Richard

; APPLICANT: Ireland, Nancy

; TITLE OF INVENTION: Lipoxxygenase Genes From Vitis Vinifera

; FILE REFERENCE: 29520/37890

; CURRENT APPLICATION NUMBER: US/09/978,522

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 60/241,220

; PRIOR FILING DATE: 2000-10-16

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4



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; LENGTH: 4237
; TYPE: DNA
; ORGANISM: Vitis LOX sequence 2
US-09-978-522-4

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Score:          3254.50  Matches: 660
Percent Similarity: 63.28% Conservative: 105
Best Local Similarity: 54.59% Mismatches: 93
Query Match:     71.78% Indels: 355
DB:              10      Gaps: 10

US-10-731-642A-1 (1-862) x US-09-978-522-4 (1-4237)

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Qy      43 GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla 62
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Qy      63 AspPro----- 64
Db      184 GATCCTGGTGAGTTTATTATTTATTTATTTTATTATTTTTCATGTTTTCATGAT 243

Qy      64 ----- 64
Db      244 GGGGTTATTGAAGTTGGGGAGAGGAGAAATGATGCCGTTTTTGTGAGGGTGAGATGGGTT 303

Qy      64 ----- 64
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Qy      65 ----- 64
Db      364 TATTCTCAGAAATTGAGTCAATGAGTTTCTTGACATCTTCCATTCAACTGGGCACTTTTC 423

Qy      65 ----- AlaAsnGly 67
Db      424 TAAGTGTCTTTGTTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTAGCAAAATGGG 483

Qy      68 LeuGlnGlyLysArgSerLysAlaIleValLeuGluAsnTrpLeuThrAsnSerThrPro 87
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Db      544 TTAACCGCGGCGAGTCTGCATTCAAGGTCAGGTCGACTGG--GATGAGGAGATTGGA 600

Qy      108 ValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhePheLeuLysSerLeu 127
Db      601 GAGCCAGGGGCATTCAATAATTAGAAACAATCACACAGTGAGTTTTTACCTCAGGACTCTC 660

Qy      128 ThrLeuGluAspValProAsnHisGlyLysValHisPheValCysAsnSerTrpValTyr 147
Db      661 ACTCTTGAAGATGTTCCCTGGACGTGGCAGAATTCACTTTGTTTGTAAATCCTGGGCTCTAC 720

Qy      148 ProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsn----- 161
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Db      162 -----GlnAlaTyrLeuProSerGluThrPro 170
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Db      901 GGGCCACTGCGCAAGTACAGAGAAGGGGAACTGGTGAATCTGAGGGAGATGGAACCGGA 960

Qy      191 LysLeuGluGluTrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspPro 210
Db      961 GAGCTTAAGGAATGGGATCGAGTGTATGACTATGCTTACTATAATGATTTGGGGAATCCA 1020

Qy      211 AspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrPro 230
Db      1021 GACAGGGATCTCAAAATACGCCCGCCCTGTGCTGGGAGGATCTGCAGAGTATCCTTATCCC 1080

Qy      231 ArgArgGlyArgThrGlyArgLysProThr-Lys----- 241
Db      1081 AGGAGGGGAAGAACTGGTAGACCACCATCTCTGAAAAAGGTAGATATTTGATGCAAAAATTC 1140

Qy      241 ----- 241
Db      1141 ATATTGTTTTCTCATGCTTTTATCATAAAAAGGATGAATATGATGATTTCTGCTCTTCTT 1200

Qy      242 -----ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTy 259
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Qy      259 rValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLe 279
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Qy      279 uLysSerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAs 299
Db      1321 GAAATCCATAGTTCAATTCTCTCTGAGTTTGAGGCTCTAIGTGACATCACCCACAA 1380

Qy      299 nGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGl 319
Db      1381 TGAGTTTGACAGCTTCCAAGATGATTAGACCTCTACGAAGGAGGAATCAAGGTCCCAGA 1440

Qy      319 nGlyProLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLe 339
Db      1441 GGGCCCTTTTACTGGACAAAATTAAAGGACAAACATCCCTCTTGAGATGCTCAAGGAACCTGT 1500

Qy      339 uArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIle-Gln----- 356
Db      1501 TCGTACTGATGGGAACATCTCTCTCAAGTTCCTCAATGCCCCAAGTCATCAAAGGTACTGC 1560

Qy      356 ----- 356
Db      1561 ATACATCTAACATCTTGTAATCTTTGAAGCCAGATTATATATATTTTTCGTAAAATT 1620

Qy      357 -----GluAspLysThrAlaTrpArgThrAspGluGluP 368
Db      1621 GATGACGTTTTTATCATGCTGGAGCAGAGGATAAGTCTGCATGGAGACCGCATGAAGAAT 1680

Qy      368 heGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArg----- 383
Db      1681 TTGCAAGAGAAAATGCTGGCTGGACTCAACCCAGTTGTCATCCG-TCTACTCCAAGTAAAC 1739

Qy      383 ----- 383
Db      1740 TACAGCTTCCTTTCAAATAATTTTAAATGCCCTGTTTGTCTTGAGAAAAATGGAACCTG 1799

Qy      383 ----- 383
Db      1800 GAAAGGCTCCAGACTTTGTTTTTCTTCCCTCCATCTACTGTCTAGCTCTTTTCTGATA 1859

Qy      384 -----LeuGlnGluPheProLysSerLysLeuAspProL 396
Db      1860 ATTATTGGCTTTTCTACTTTGTTTGCAGGAGTTTCTCTCCAAAAGCAAGCTGGATCCTG 1919

Qy      396 ysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspG 416
Db      1920 AAGTTTATGGCAACCAACAGTTTCAATAAACCAAGACACATAGAGAATCACCTGGATG 1979
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Qy	416	lyLeuThrIleAspGluAla	-----	-----	-----	422
Db	1980	ACCTTACTATAAACGAGGT-AACGCTCTTAGGTTCCCTCTTTTCAGACTAAATTTTCAA	2038			
Qy	422	-----	-----	-----	-----	422
Db	2039	TGTCGACATGTTAAATTTTTCATTTGGAACACAAAGCCATAGTAACAGAAATGGTGCTT	2098			
Qy	423	-----IleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetP	439			
Db	2099	TTTACTAGGCAATGGAGAAGAGGCTATTTCATATTAGATCACCATGATGTTTCATGC	2158			
Qy	439	roTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuL	459			
Db	2159	CATACCTGAGGAGATAACACA--ACTTCCACGAAAACTTATGCCTCAAGGACTCTCC	2215			
Qy	459	eupheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisP	479			
Db	2216	TCTTCCTGAAAGACGACGGAACCTTTGAAGCCACTGGCGATTGAATTGAGCCTACCACATC	2275			
Qy	479	roAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValG	499			
Db	2276	CTAGTGGGGATAAAATTTGGAGCTGTCAACAAAGTATATACGCCAGCTGAAATGGTGTG	2335			
Qy	499	luGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisG	519			
Db	2336	AAGGTTCCATTTGGCAGCTGGCTAAAGCTTATGTCTGTGAATGACTCTGGCTATCATC	2395			
Qy	519	lnLeuIleSerHisTrpLeu	525			
Db	2396	AGCTCCTCAGCCACTGGTA-TGTAATATCCCAAGAAAGTGAATACAGTTTGGGCTTAA	2454			
Qy	526	-----	-----	-----AsnThrHisAlaAlaI	531	
Db	2455	ATCTGAAGCGGGTTGTGAATATCTTTGATGTTGGTTGCAGGTTGAATACACATGCTGCAA	2514			
Qy	531	leGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysL	551			
Db	2515	TTGAGCCATTTGTGATTGCAACCAACAGGCAGCTCAGCGTGCTTCATCCAAATTCACAAGC	2574			
Qy	551	euLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuI	571			
Db	2575	TTTTTGCAATCCTCACTTCGCTGATACAAATGAATATAAAATGCATTAGCTCGACAAATCCTCA	2634			
Qy	571	leAsnGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetS	591			
Db	2635	TCAAATGCTGGTGGAGTGGTGAGAGCACAGTTTTTCCATCAAAGTATGCCATGGAAATGT	2694			
Qy	591	erAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleL	611			
Db	2695	CATCTGTTGTTTACAAAGACTGGGTCTTACTAGCAAGCACTTCCTGCTGATCTCATCA	2754			
Qy	611	ys	-----	-----	-----	611
Db	2755	A-GAGGTATATAATACTGTTAGTGATTGTTTTCTTCCTGCTGTGGAATGAATCTAGTG	2813			
Qy	612	-----	-----	-----ArgGlyVala	615	
Db	2814	AAAAATTGTGATTTTCATCTAACTGATATGCTGCAACTTGGGCACACTCTTTTCAGAGGAATGG	2873			
Qy	615	laValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrA	635			
Db	2874	CGGTTGAGGAATTCAGAGGCTCCTCATGGACTCCGCTACTGATAGATGACTACCCCTATG	2933			
Qy	635	laValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnT	655			
Db	2934	CTGTTGATGGACITTGAGATCTGGTCAGCTATTGAGACATGGGTGAAAGAGTATTGCTCAT	2993			
Qy	655	yrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysG	675			
Db	2994	TCTACTACAAGACAGATGAGATGGTCCAGAAAGACTCTGAGCTTCAGTCTCTGGTGAAGG	3053			

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Qy 675 luLeuArgGluGluGlyHisGlyAspLysLysAspGluProTfTpProLysMetGlnT 695
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Db 3054 AAGTCAGGAAGAGGGTCATGGCGACAAGAAGGACGAGCCCTGGTGGCTAAAAATGCATA 3113
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Qy 695 hrValGlnGluLeuIleAspSerCysThrIleThrIleAlaSerAlaLeuHisa 715
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Db 3114 CTGTCAAGAGCTGATAGAAACATGCACCATTATCATCTGGGTGGCTTCTGTCTCCATG 3173
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Qy 715 laAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuS 735
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Db 3174 CTGCAGTGAATTCGGGCAGTACCCCTTATGCAGGCTACCTCCCAAAACGCCCAACGATAA 3233
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Qy 735 erArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProA 755
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Db 3234 GCCGCAGATTTCATGCCTGAAGAAGGCACTCCTGAGTATGAAGAACTCAAGTCCAATCCTG 3293
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 755 spLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuI 775
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Db 3294 ATAAGGCTTTCCTGAAACAATCACTGCCAGCTGCAGACCCCTTCTTGGCATCTCCCTTA 3353
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Qy 775 leGluIleLeuSerArgHisSerAspThrLeuTyrLeuGlyGlnArgGluSerProG 795
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Db 3354 TTGAGGTCCTTTCCAGGCATTCCTCCGATGAGGTTTATCTTTGGACAGAGACACTCCTG 3413
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Qy 795 luTfTpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSera 815
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 3414 AATGGACCCTGGACACACACCATTTGAAAGCTTTTGAGAAATTCGGAAGGAAGCTGGCAG 3473
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Qy 815 spIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyP 835
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Db 3474 ACATTGAAGAAATGATCATAGATAGAAATGGAAATGAGAGATTCAAGAACACAGATTGGGC 3533
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Qy 835 roValLysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysG 855
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Db 3534 CTGTGAAGATACCATACACACTGCTCTACCCCAAGCGAAGGTGGGCTTACTGGCAAAG 3593
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 855 lyIleProAsnSerValSerile 862
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Db 3594 GGAATCCCAACAGTGTCTCCATC 3616
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RESULT 4
US-09-938-842A-1504
; Sequence 1504, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1504
; LENGTH: 2580
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1504

Alignment Scores:
Pred. No.: 0 Length: 2580
Score: 3202.50 Matches: 595
Percent Similarity: 82.79% Conservative: 122
Best Local Similarity: 68.71% Mismatches: 138
Query Match: 70.63% Indels: 11

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DB:	9	Gaps:	7
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QY	1	MetPheLeuGluIysIleValAspAlaIleThrGly-----LysAspAspGlyLys	17
DB	1	ATGTTCGGAGAA---CTTAGGGATCTGCTACCGGCGGGAATGAGACGACGAAG	57
QY	18	LysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsn	37
DB	58	AAGGTGAAGGAACGGTGTCTGATGAAGAAGAACGTCCTCGATTTCACGATTTCAT	117
QY	38	AlaSerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIle	57
DB	118	GCTTCGTTTCTCGATCGTCTTCATGAATTTCTCGAAACAAATCACTCTTCGTCTT	177
QY	58	SerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyr	77
DB	178	AGCTCTGATGTTACTGATTCAGAAAACGGTTCTAAAGGCAAACTAGGGAAGGCTG	237
QY	78	LeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgVal	97
DB	238	TTGGAGGATTGGATCACAACAATCACGTCGTAAACCGCAGGCGAATCCGCTTTC	297
QY	98	ThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeu	117
DB	298	ACGTTTCGATTAC---GAAACCGATTTCGGTTACCTTGAGCATTTCTTGATCAGA	354
QY	118	HispheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLys	137
DB	355	CATTTTCAGTGAGTTCTTCTCAAAAGTCTCACACTTGAAGACGTTTCCAGGCCAT	414
QY	138	ValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIle	157
DB	415	GTCCATTACATCTGTAATTCTTGGATTTACCTTGCTAAACACTACACTACAGAC	474
QY	158	PhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArg	177
DB	475	TTCTTCTCCAACAAGACTTATCTTCCACATGAACAACCCAGCGACGCTGCTCA	534
QY	178	GluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArg	197
DB	535	GAAGAAGAGCTAGTGAGTTTGAGAGGAACCGCGGAAGGAGAGCTTAAGGAATG	594
QY	198	ValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSer	217
DB	595	GTATATGACTATGCTTACTACATGATTTAGGCGTCCCACCAAGAAC-----	645
QY	218	ArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArg	237
DB	646	CGGCCTGTACTTGGAGGGACACAGGAGTATCCTTACCCAAAGAGGAAGAAC	705
QY	238	LysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAsp	257
DB	706	AAACCAACTAAAGAAGATCCTCAAACCGAGAGCAGGCTACCGATCACATCGAG	765
QY	258	IleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPhe	277
DB	766	ATATATGTTCCACGAGATGAGAGATTTGGACACTTGAAGATGTCTGATTTCTT	825
QY	278	AlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThr	297
DB	826	GCTCTAAAGCGATTGCTCAGTTTCATCCCACTGCACTTGAGGCTGTATTGACG	885
QY	298	HisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeu	317
DB	886	CCTAAAGAGTTTGATTCTTTTGAAGATGTTCTTAAGATCTATGAAGAAGGAAT	945
QY	318	ProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGlu	337
DB	946	CCAAACCAAGCTTTGATTGATAGTATCGTTAAGAATAATACCGCTTGAGATGT	1005
QY	338	LeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGlu	357

DB	1006	ATATTCAACACAGATGGCCAGAAATTCCTTAAGTTTCCAGTGCCTCAGGTCAACAAGAG	1065
QY	358	AspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsn	377
DB	1066	GACAAAACCTGCATGGAGAACAGATGAGGAATTTGCTAGAGAAATGTTGGCTGGA	1125
QY	378	ProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIle	397
DB	1126	CCTGTTGTTATTCAACTTCTTAAGGAGTTTCCTCCAAAGAGTAAGCTTGACAGTGA	1185
QY	398	TyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeu	417
DB	1186	TACGGTAACCAGAACAGTACAATCACTAAAAGCCACATAGAACACAATTTGGATG	1245
QY	418	ThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIleLeu	437
DB	1246	ACTGTTGAAGAGGCTCTGGAGAAGGAGAGGTTGTTTATATTAGACCCACCATG	1305
QY	438	MetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThr	457
DB	1306	ATGCCATACTTGGGACGCGTAAACACACCACG---ACCAAGACTTATGCAAGCAG	1362
QY	458	LeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuPro	477
DB	1363	CTTCTGTTCTTGAAGATGATGGGACCTTGAAGCCGTTGGTGATAGAGCTGAGCTT	1422
QY	478	HisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGly	497
DB	1423	CATCCTAATGGAGACAAATTTGGAGCAGTGAGTGAAGTATATACGCCCTGGT---	1479
QY	498	ValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyVal	517
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QY	518	HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAla	537
DB	1540	CATCAGCTTATTAGCCACTGGATGCAACACACACGCATCGATTGAACCGTTTGTG	1599
QY	538	ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg	557
DB	1600	ACAAACAGACAGCTGAGTGTCTTCCACCGGCTCTTTAAGCTCCTTGAACCTC	1659
QY	558	GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeu	577
DB	1660	GATACGATGAATATCAATGCACTTGCTAGGCAAAATCTTGATCAATGGTGGTATA	1719
QY	578	GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp	597
DB	1720	GAAATCACTGTGTTTCTTCTTAAATACGCCATGGAGATGTCACTCTTCATTACA	1779
QY	598	---TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal	616
DB	1780	CACCTGGACCTTCCCTGACCAAGCATTACCAGCAGAACTTAAAAAGAGAGGGAT	1839
QY	617	GluAspSerSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal	636
DB	1840	GAGGATCCAGAAGCACCAACACGGATTACGTCTGAGGATAAAAGACTATCCTTAC	1899
QY	637	AspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyr	656
DB	1900	GATGGCTTGAGGTTTGGTATGCTATTGAATCATGGGTCCGAGACTACATTTCTT	1959
QY	657	TyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeu	676
DB	1960	TACAAGATAGAGGAGGATATCCAAACCGACACAGAGCTCCAAGCCTGGTGAAGG	2019
QY	677	ArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrVal	696
DB	2020	CGCGAGGAAGGTCATGGAGACAAAAAGTCAGAACCATGGTGGCTTAAATGCAAC	2079
QY	697	GlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAla	716



Db 2080 GAAGAACTGTTGAGTCTTGACCATCATATTATTGGGTGGCTTCTGCTCTTCATGCAGCT 2139

Qy 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736  
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Db 2140 GTTAACTTCGGACAGTATCCAGTTGCTGGGTACCTCCCAAACAGACCGACTATAAGCCGT 2199

Qy 737 AsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLys 756  
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Db 2200 CAGTACATGCCAAAGGAAACACTCCAGAGTTTGAAGAACTTCAGAAGAAATCCTGTATAAA 2259

Qy 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776  
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Db 2260 GTGTTTTGAAGACCATCACAGCTCAGCTTCAGACACTTCTAGGGATATCTCTGATTGAG 2319

Qy 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrp 796  
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Db 2320 ATTCTCTACTATTCTAGCGACGAGGTCTATTTTGGGACAGAGAGATTCTAAAGAATGG 2379

Qy 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle 816  
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Db 2380 GCGGCTGAGAAAGAAGCGTTGGAGCGGTCGAGAAGTTTGGAGAGAAAGTAAAGGAGATT 2439

Qy 817 GluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProVal 836  
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Db 2440 GAGAAGAACATTGATGAGGGAACGACGACGAGACTCTCAAGAACAGGACTGGTTTGGTT 2499

Qy 837 LysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856  
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Db 2500 AAGATGCCATACACTTTATTGTTCCGAGCAGTGAAGGGCGGAGTCACGGCAGGGGATT 2559

Qy 857 ProAsnSerValSerIle 862  
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Db 2560 CCAATAGCGTCTCTATC 2577

RESULT 5

US-09-938-842A-1504

; Sequence 1504, Application US/09938842A

; Publication No. US20040009476A9

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPT300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1504

; LENGTH: 2580

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1504

Alignment Scores:

Pred. No.:	0	Length:	2580
Score:	3202.50	Matches:	595
Percent Similarity:	82.79%	Conservative:	122
Best Local Similarity:	68.71%	Mismatches:	138
Query Match:	70.63%	Indels:	11
DB:	11	Gaps:	7

US-10-731-642A-1 (1-862) x US-09-938-842A-1504 (1-2580)

Qy 1 MetPheLeuGluLysIleValAspAlaIleThrGly-----LysAspGlyLys 17  
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Db 1 ATGTTTCGGAGAA---CTTAGGGATCTGTCTACCGGGCGGGAATGAGACGACGAGAAG 57

Qy 18 LysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsn 37  
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Qy 38 AlaSerValLeuAspGlyValValLeuGluPheLeuGlyArgValSerLeuGluLeuIle 57  
|||||  
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Qy 58 SerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyr 77  
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Db 178 AGCTCTGATGTTACTGATTCAGAAAACGGTTCTAAAGGCAAACTAGGGAAGGCTGCTCAC 237

Qy 78 LeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgVal 97  
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Db 238 TTGGAGGATTGGATCACAAATCACGTCGTTAAACCGAGCGGAATCCGCTTTTCAAGGTC 297

Qy 98 ThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeu 117  
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Qy 118 HisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLys 137  
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Qy 138 ValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIle 157  
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Qy 158 PhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArg 177  
|||||  
Db 475 TTCTTCTCCAACAAGACTTATCTTCCACATGAACAACCCAGCGACGCTGCTCAAGTATAGA 534

Qy 178 GluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArg 197  
|||||  
Db 535 GAAGAAGAGCTAGTGAGTTTGAGAGGAACCCGGCGAAGGAGAGCTTAAGGAATGGGACAGA 594

Qy 198 ValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSer 217  
|||||  
Db 595 GTATATGACTATGCTTACTACAAATGATTTAGCGCTCCCAACCAAGAAC-----CCA 645

Qy 218 ArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArg 237  
|||||  
Db 646 CGGCTGTACTTGGAGGGACACAGAGTATCCTTACCCCAAGAGAGGAAGAACCGGGCGG 705

Qy 238 LysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAsp 257  
|||||  
Db 706 AAACCAACTAAAGAAGATCCTCAACCGAGAGCAGGCTACCGATCACATCGAGCCTAGAC 765

Qy 258 IleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPhe 277  
|||||  
Db 766 ATATATGTTCCACGAGATGAGAGATTGGACACTTGAAGATGTCTGTGATTTCTTCTTAT 825

Qy 278 AlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThr 297  
|||||  
Db 826 GCTCTAAAAGCGATTGCTCAGTTTCATCCAACCTGCACCTTAGGCGTGTATTTCGACGATACT 885

Qy 298 HisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeu 317  
|||||  
Db 886 CCTAAAGAGTTTGATTCTTTGAAGATGTTCTTAAGATCTATGAAGAAGGAATCGATCTA 945

Qy 318 ProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGlu 337  
|||||  
Db 946 CCAAAACCAAGCTTTGATTGATAGTATCGTTAAGAATATACCGCTTGAGATGTTAAAGGAG 1005

Qy 338 LeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGlu 357  
::: |||  
Db 1006 ATATTCAAGAACAGATGGCCAGAAATTCCTTAAGTTTCCAGTCGCTCAGGTCATCAAGAG 1065

Qy 358 AspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsn 377  
|||||  
Db 1066 GACAAAACCTGCATGGAGAACAGATCAGGAATTTGCTAGAGAAATGTTGGCTGGACTAAAC 1125



Db 193 GATCCTGGTGAGTTTTTTTTTTTTTTTTTTTTCCTTCATGTTTTTGATGCGGTTGTTG 252  
Qy 64 ----- 64  
Db 253 AAGTTGGAGGAGAGGAGTTGTATACCGTTTTTGTGAGGGTGAGATGGGTTCTGAATTTGA 312  
Qy 64 ----- 64  
Db 313 TGATAGCAATTGGAAAAAGATGTGATTTTTTGGAAAGAGGCCAAGAGGGGTTGTTATTCTCA 372  
Qy 64 ----- 64  
Db 373 GAGATGAGTCAAAATGACTTTCTTGACATCTTCCATTCAACTGGGCACCTTTTCTAACTGCT 432  
Qy 64 ----- 64  
Db 433 TTTGTTTTTGTGTTTTTGTGTTTTTAATGCTTTTGTGTTTTCTACTCTTTCTCTGTTTATAT 492  
Qy 64 ----- 64  
Db 493 TTCTTTTTCATCAACCACCTATACATGCCACCTAACTCAATATGAAATTCCCATGCAGCTG 552  
Qy 64 ----- 64  
Db 553 CCCTTTTTTTAAGCCACTAGATCTTGGGTGATTTTTTTTAGTCTTAGATCTTGGGTTAGAT 612  
Qy 64 ----- 64  
Db 613 TTCCCCAGATTTTCACAAAAGTTGAAACTGAAATTCATAAAAATTTTGTGAGGATCACTCCTG 672  
Qy 64 ----- 64  
Db 673 TTGGAGTTAAAGAGAAAGAAATTGCCATAAACCAAGGAGATGAATGTTGTGAAATATTTC 732  
Qy 64 ----- 64  
Db 733 TCAAAACTTCATCATCAAAATACCTGCCAAAAACAGCCACAGTTTCTGAAATTTTCATGCAGC 792  
Qy 64 ----- 64  
Db 793 AAAGCCACTGCTGCTTGTAGCAAGTCCAAGCTCAAAACATAAAAGCCTTTTCAACCCAGTG 852  
Qy 64 ----- 64  
Db 853 ATTTTGTGAATAACATGTAAAAATGCAGTGACCATCTGTGTAGTGATGATATTGAACTTG 912  
Qy 65 -----AlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAs 80  
Db 913 TGTGCCTTTTGTAGCAAAATGGGTTACAGGGGAAACTTGGGAAACCAGCATACTTTGGAAGA 972  
Qy 80 nTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAs 100  
Db 973 CTGGATTACCAACAATTACTTCTTTAAACGCTGGCGAGTCTGCATTCAGGTCAAGTTCGA 1032  
Qy 100 pTrpAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSe 120  
Db 1033 CTGG---GATGAGGAGATTGGAGAGCCAGGGGCATTCTATAATTAGAAACAATCACCACAG 1089  
Qy 120 rGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPh 140  
Db 1090 TGAGTTTTTACCTCAGGACTCTCACTCTTGAAGATGTTCTCGGCGTGGCAGAATTCACIT 1149  
Qy 140 eValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAl 160  
Db 1150 TGTTTGTAAATTCCTGGGTCTACCCCTGCTAAGCACTACAAAACACTGACCGTGTTCCTTCA 1209  
Qy 160 aAsn----- 161  
Db 1210 TAATCAGGTAAGACTAATTTGCTTGATAGTAGGAGATCTGCTGTGGCATTTGTGCCCAT 1269  
Qy 162 -----GlnAl 163  
Db 1270 TGAGCTTAGGCAAGGAGAAATTGCTGCTFAAAGGAATGTGTTTATTTATCTGCTGCAGAC 1329

Qy 163 aTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValTh 183  
Db 1330 ATATCTTCCAAAGTGAAACACAGGGCCACTGCGCAAGTACAGAAAAGGGGAACGTGGTGA 1389  
Qy 183 rLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArgValTyrAspTyrAlaTy 203  
Db 1390 TCTGAGGGGAGATGGAAACCGAGAGCTTAAGGAATGGATCGAGTGTATGACTATGCTTA 1449  
Qy 203 rTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGl 223  
Db 1450 CTATAATGATTTGGGAAGCCAGACAGGGATCTCAAAATATGCCCGCCTGTGCTGGGAGG 1509  
Qy 223 ySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys----- 241  
Db 1510 ATCTGCAGAGTATCCTTATCCAGAGGGGAAGAACTGGTAGACCACCATCTGAAAAAGG 1569  
Qy 241 ----- 241  
Db 1570 TAGATATTTGATACACAAATTCATATTGTTTCTCATGCTTTTATCATAAAGGATGAATA 1629  
Qy 242 -----ThrAspProAsnSerGluSerArgIleProLe 252  
Db 1630 TGATTGATTTCTGCTCTTCTTTTAAATTAACAGATCCCAAAACTGAGAGCAGATTGCCACT 1689  
Qy 252 uLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSe 272  
Db 1690 TGTGATGAGCTTAAACATATATGTTCCAAGAGATGAACGATTTGGTCACCTGAAGATGTC 1749  
Qy 272 rAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuProGluPheLysAl 292  
Db 1750 AGACTTCTGGCTTATGCCCTGAAATCCATAGTTCAATTCCTTCTCCTGAGTTTGAGGC 1809  
Qy 292 aLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGl 312  
Db 1810 TCTATGTGACATCACCCCAATGAGTTTGACAGCTTCCAAGATGTATTAGACCTCTACGA 1869  
Qy 312 uGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLe 332  
Db 1870 AGGAGGAATCAAGGTCCAGAGGGGCCCTTTACTGGACAAAAATTAGGACAACATCCCTCT 1929  
Qy 332 uGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrPr 352  
Db 1930 TGAGATGCTCAAGGAACCTTGTCTGATCCGATGGGGAACATCTCTTCAAGTTCCCAATGCC 1989  
Qy 352 oGlnValIle-Gln----- 356  
Db 1990 CCAAGTCATCAAAGGTACTGCATACATCTAAACATCTTGAATCTTTGAAGCCAGATTAT 2049  
Qy 357 -----GluAspLysThrA 361  
Db 2050 ATATTTATTTTTCATAAAATTTGATGACGTTTTTATCATGCTGGAGCAGAGGATAAGTCTG 2109  
Qy 361 laTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleI 381  
Db 2110 CATGGAGGACTGACGAAGAATTGCTAGAGAAATGCTGGCTGGACTCAACCCAGTTGTCA 2169  
Qy 381 leSerArg----- 383  
Db 2170 TCCG-TCTACTCCAAGTAAACTACAGCTTCCTTTCAAATAATTTTAAATGCCCTGTTGT 2228  
Qy 383 ----- 383  
Db 2229 TTTCTGAGAAAAATGGAACTTGGAAAGGCTTCCAGACTTTTGTGTTTCTTTCCCTCCATCTAC 2288  
Qy 384 -----LeuGlnGluPheProp 389  
Db 2289 TGTTCTAGCTCTTTTCTGATAATATTGGCTCTTTCTACTTTTGTGTTTGTGTTGAGGAGTTTCTC 2348  
Qy 389 roLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluG 409  
Db 2349 CAAAAAGCAAGCTGGATCCTGAAGTTTATGGCAACCAAAACAGATTCAATAACCAAGAAC 2408



QY 409 lnIleGluAspLysLeuAspGlyLeuThrIleAspGluAa----- 422  
Db 2409 ACATAGAGAATCACCTGGATGACCTTACTATAAACGAGGT-AACGCTCTTAGGTTCCGTT 2467  
QY 422 ----- 422  
Db 2468 CTTTCAAACATAAATTTTCAATGTCGACATGTTAATTTTTCATTTGGAACACAAGCCAT 2527  
QY 423 -----IleLysThrAsnArgLeuPheIleLeuA 432  
Db 2528 AGTAACTGAAAAATGGTGCTTTTACTAGGCAATGGAGAAGAGGCTATTATATAG 2587  
QY 432 snHisHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysT 452  
Db 2588 ATCACCATGATGTTTTCATGCCATACCTGAGGAGATAAACACA---ACTTCCACGAAA 2644  
QY 452 hrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaI 472  
Db 2645 CTTAGCCTCAAGGACTCTCCTCTCTCTGAAAGACGACGGAACCTTTGAGCCACTGGCGA 2704  
QY 472 leGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrT 492  
Db 2705 TTGAATTGAGCCTACACATCCTAATGCGGATAAATTCGGAGCTGTCAACAAAGTATACA 2764  
QY 492 hrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaV 512  
Db 2765 CACCAGCTGAAGATGGCGTTGAAGGTTCCATTGGCAGCTGGCTAAGCTTATGCTGTG 2824  
QY 512 alAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeu----- 525  
Db 2825 TGAATGACTCTGGCTATCATCAGCTCCTCAGCCACTGGTA-CGTAATCTCCCAAGGAAA 2883  
QY 525 ----- 525  
Db 2884 GTGGGTACAGTTGGGGCGGTAAATCTGAAGCGGGTTATGAATATCTTTGATGTTGGTTGCA 2943  
QY 526 -----AsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerA 544  
Db 2944 GGTGTAATACATGCTGCAATTTGAGCCATTTGATGATTGCAACCAACAGGCAGCTCAGTG 3003  
QY 544 laLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnA 564  
Db 3004 TGCTTCACCCAATTCACAAGCTTTTGCACTCCTCCTCCTGATACGATGAATATAAATG 3063  
QY 564 laLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuThrValPheProA 584  
Db 3064 CATTAGCTCGACAATCCTCATCAATGCTGGTGGAGTGGTGGAGACACAGTTTTTCCAT 3123  
QY 584 laLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPheProGluGlnA 604  
Db 3124 CAAAGTATGCCATGGAAATGTCTATCTGTTGTTTACAAAGACTGGGTTCTCACTGAGCAAG 3183  
QY 604 laLeuProThrAspLeuIleLys----- 611  
Db 3184 CACTTCTGCTGATCTCATCAA-GAGGTATATAAAATACTGTTAGTGATGTTTCTTTTCC 3242  
QY 611 ----- 611  
Db 3243 TGCTGTGCAATGAATCTAGTGAAATTTGTGATTTTCATCTAACTGATATGCTCCAAC TTG 3302  
QY 612 -----ArgGlyValAlaValGluAspSerSerSerProLeuGlyIleArgLeuL 628  
Db 3303 GGCACCTCTTCAGAGGAATGGCGTTGAGGATTCAGAGGCCCTTCATGGACTCCGCCTAC 3362  
QY 628 euIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerT 648  
Db 3363 TGATAGATGACTACCCCTATGCTGTTGTGAGACTTGAGATCTGGTCAGCTATTGAGACAT 3422  
QY 648 rpValThrGluTyrCysAsnTyrTyrLysSerAspAlaValGlnLysAspThrG 668  
Db 3423 GGGTGAAGAGTATTGCTCTACTACAAGACAGATGAGATGGTCCAGAAAGACTCTG 3482  
QY 668 luLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHisGlyAspLysLysAspGluP 688

Db 3483 AGCTTCAGTCTGTTGGTGAAGGAAGTCAGGGAAGAGGGTTCATGGCGACAAGAAGGACGAGC 3542  
QY 688 roTrpTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIleT 708  
Db 3543 CTTGGTGGCTAAATCGCTACTGTCAAAGAGCTGATAGAAACATGACCATTATCATCT 3602  
QY 708 rpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrL 728  
Db 3603 GGGTGGCTTCTGCTCTCCATGCTGCAAGTGAATTTTCGGGCGAGTACCCCTATGACAGGTACC 3662  
QY 728 euProAsnArgProThrLeuSerArgAsnPheMetProGluProGlySerProGluTyrG 748  
Db 3663 TCCCAACCGCCCAACGATAAGCCGAGATTTCATGCCTGAAGAGGCACTCCTGAGTATG 3722  
QY 748 luGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGlnT 768  
Db 3723 AAGAACTCAAGTCCAATCCTGATAAGGCTTTCCTGAAAAACAATCACTGCCAGCTGCAGA 3782  
QY 768 hrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHisSerSerAspThrLeuTyrL 788  
Db 3783 CCCTTCTTGGCATCTCCCTTATTGAGTCCCTTCCAGGCATTCTCCGATGAGGTTTATC 3842  
QY 788 euGlyGlnArgGluSerProGluTrpThrLysAspGlnGluProLeuSerAlaPheAlaA 808  
Db 3843 TTGGACAGAGAGACACTCCTGAATGGACCCCTGGACACAACCATTGAAAGCTTTTGAGA 3902  
QY 808 rgPheGlyLysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGluL 828  
Db 3903 AATTCCGAAGGAAGCTGGCAGACATTGAAGAAATGATCATAGATAGAAAATGGAATGAGA 3962  
QY 828 ysTrpLysAsnArgSerGlyProValLysValProTyrThrLeuLeuPheProThrSerG 848  
Db 3963 GATTCAAGAACAGAGTTGGGCCCTGTGAAGATACCATACACACTGCTCTACCCACAAGCG 4022  
QY 848 luGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862  
Db 4023 AAGTGGGCTTACTGGCAAAGGGATTCCCAACAGTGTCTCCATC 4066

RESULT 7

US-10-425-114-11204  
; Sequence 11204, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 11204  
; LENGTH: 2828  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701040644\_FLI

US-10-425-114-11204

Alignment Scores:  
Pred. No.: 0 Length: 2828  
Score: 3104.50 Matches: 578  
Percent Similarity: 82.18% Conservative: 123  
Best local Similarity: 67.76% Mismatches: 139  
Query Match: 68.47% Indels: 13  
DB: 17 Gaps: 8

US-10-731-642A-1 (1-862) x US-10-425-114-11204 (1-2828)

QY	17	LysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAsp	116	AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis	135	
Db	52	AAGAGGGTTAAAGGAGAGAGTGGTTTGTGATGAAGAAGGGTGTGTGGACTTCCACGACATC	111	343	AACAATCACCATAGCCAGTTCTACCTCAAGACACTGACCATTTGAAGACATTCACAGGCAT	402
QY	37	AsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeu	56	136	--GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSer	154
Db	112	AAAGCCAACGTTCTCGATCGAGTTTACAGAGTTATTAGGCAAGGGTGTCTCTCTTCAGCTT	171	403	GATGGTCTCTGTTAAATTTGTCTGCAATTCITGGGTCTACCCCTGCTCATCGTTACGCCCAT	462
QY	57	IleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAla	76	155	AspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArg	174
Db	172	ATTAGTGCTACTACTCTCGATCCAGCAAGGGGTTA-----TTGAGAGGGAAGGTGGCA	225	463	GATCGTGTCTTCTTGGCCAAACAAGGCTTATCTTCCATGTATACACACCTGAGCCACTGCGC	522
QY	77	TyrLeuGluAsnTrpLeuThrAsnSerThrProIle--AlaAlaGlyGluSerAlaPhe	95	175	LysTyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGlu	194
Db	226	AAC TTGGAGAGGTGGGTTTCGACGATTACCTCTTTTGACATCAACAACAGACACAGAGTTTC	285	523	AAGTTCAGGGAACAAGAAGTAACTCTCTCGGGAAGGGTTCGGGAAGCTTAATGAG	582
QY	96	ArgValThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleLys	115	195	TrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGln	214
Db	286	TCAGTTACATTTGAGTGG--GATGAGAGCATGGGTGTCTCTGGGCAATTCATAATCCGA	342	583	TGGGACAGAGTCTATGACTATGCATCTACATGATTTGGGACTTCCAGATGATGGTCTCT	642
QY	116	AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis	135	215	AspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArg	234
Db	343	AACAATCACCATAGCCAGTTCTACCTCAAGACACTGACCATTTGAAGACATTCACAGGCAT	402	643	GACTATGCACGCCCTGTCTCTGGAGGA--TCACAATTTCCATATCCACGTAGAGGAAGA	699
QY	136	--GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSer	154	235	ThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMet	254
Db	403	GATGGTCTCTGTTAAATTTGTCTGCAATTCITGGGTCTACCCCTGCTCATCGTTACGCCCAT	462	700	ACTAGTCGTCCACATTTGCAAAACAGATCCTAAAACTGAGTCAAGATTGCATCTTCTA---	756
QY	155	AspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArg	174	255	SerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPhe	274
Db	463	GATCGTGTCTTCTTGGCCAAACAAGGCTTATCTTCCATGTATACACACCTGAGCCACTGCGC	522	757	AATCTAAACGTTATGTGCCGAGGATGAACAGTGTGGCCATGTCAAGTTTTTCAGATTTT	816
QY	175	LysTyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGlu	194	275	LeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPhe	294
Db	523	AAGTTCAGGGAACAAGAAGTAACTCTCTCGGGAAGGGTTCGGGAAGCTTAATGAG	582	817	CTGGCTTACTCTCTGAAATCTGTTGCTCAGGTTTGTCTTCCAGAGATTAAATCTTTGTGT	876
QY	195	TrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGln	214	295	AspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyGly	314
Db	583	TGGGACAGAGTCTATGACTATGCATCTACATGATTTGGGACTTCCAGATGATGGTCTCT	642	877	GACAAAACATAATGAGTTTGACACCTTTCAAGATGTACTTGATATTTATGAGGGAAGT	936
QY	215	AspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArg	234	315	IleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIle	334
Db	643	GACTATGCACGCCCTGTCTCTGGAGGA--TCACAATTTCCATATCCACGTAGAGGAAGA	699	937	ATTAAGCTGCCAAGTGGACCTTTAACGAGTAAACTGAGAAAACTTGTTCCTATGAGCTA	996
QY	235	ThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMet	254	335	LeuLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIle	354
Db	700	ACTAGTCGTCCACATTTGCAAAACAGATCCTAAAACTGAGTCAAGATTGCATCTTCTA---	756	997	TTGCGAGAACTTATTAGGAATGATGGTGAGAGATTCTCTCAAAATTCCTCCGTCGCTGATGTG	1056
QY	255	SerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPhe	274	355	IleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAla	374
Db	757	AATCTAAACGTTATGTGCCGAGGATGAACAGTGTGGCCATGTCAAGTTTTTCAGATTTT	816	1057	ATCAAAGTGTAAAGACAGCATGGAGGACAGATGAGGAATTTGCAAGGGGAATGCTTGCA	1116
QY	275	LeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPhe	294			
Db	817	CTGGCTTACTCTCTGAAATCTGTTGCTCAGGTTTGTCTTCCAGAGATTAAATCTTTGTGT	876			
QY	295	AspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyGly	314			
Db	877	GACAAAACATAATGAGTTTGACACCTTTCAAGATGTACTTGATATTTATGAGGGAAGT	936			
QY	315	IleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIle	334			
Db	937	ATTAAGCTGCCAAGTGGACCTTTAACGAGTAAACTGAGAAAACTTGTTCCTATGAGCTA	996			
QY	335	LeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnVal	354			
Db	997	TTGCGAGAACTTATTAGGAATGATGGTGAGAGATTCTCTCAAAATTCCTCCGTCGCTGATGTG	1056			
QY	355	IleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAla	374			
Db	1057	ATCAAAGTGTAAAGACAGCATGGAGGACAGATGAGGAATTTGCAAGGGGAATGCTTGCA	1116			

Qy	375	GlyValAsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAsp	394
Db	1117	GGGGTTAAACCCCTGTTATTATCCGGCGTCTCCAAGAAATTTCCCCCGGCAGCAAACTAGAC	1176
Qy	395	ProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeu	414
Db	1177	CCCAGCGTATATGGAGACCAAACTAGCTCCATCAGAGCAACGCACATAGAAAATAGTTTG	1236
Qy	415	AspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHis	434
Db	1237	GATGGCGTTACAATAGACGAGGCAATTCAAAATATGAGGCTATTATATATTAGATCATCAC	1296
Qy	435	AspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAla	454
Db	1297	GACTCGTTGATGCCATACATTAGTCGAATAAAC--TCTACCAACACAAAAGACTTATGCC	1353
Qy	455	SerArgThrLeuLeupheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeu	474
Db	1354	TCTAGAACGCTCCTGTTTCTACAAGATGACGGTACACTCAAGCCACTGGCTATAGAGTTA	1413
Qy	475	SerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAla	494
Db	1414	AGCTTACCCCATCCACAAGGGGAACAACATGGAGCTGTGAGCAAAAGTTTTCACCTCCAGCA	1473
Qy	495	AspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaValAsnAsp	514
Db	1474	CAAGAAGGAGTATCGGCTTCGGTGTGGCAGCTGGCTAAGGCTTATGCAGCCGTCAATGAT	1533
Qy	515	SerGlyValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPhe	534
Db	1534	TCAGGATATCATCAATTGGTTAGCCACTGGTTATACACTCACCGCAGTAATTGAACCGTTC	1593
Qy	535	ValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisPro	554
Db	1594	ATTATAGCCACAAAACAGGCAGTTGAGTATTCTTCACCCCAATACACAAAGCTCTTGAAGCCA	1653
Qy	555	HisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGly	574
Db	1654	CACCTCAGGGACACAATGCATATAAATGCCTTAGCCCGGCACACGCTCATCAATGCTGGA	1713
Qy	575	GlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValVal	594
Db	1714	GGGGTACTAGAGATTACAGTTTCCCTGGTAAATTCGCCCTGGAAATGTCGTCGGTTATA	1773
Qy	595	TyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyVal	614
Db	1774	TACAAAAGTTGGGTATTACCCGAGCAGGCACACTACCTGCTGATCTTCTTAAGAGGGGAATG	1833
Qy	615	AlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyr	634
Db	1834	GCAATTCCTGATTCAAGTTCTCGTTCATGGACTAAGGCTTGTGATAGAGGATTATCCGTTT	1893
Qy	635	AlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsn	654
Db	1894	GCCGTGGACGGCATAGAAATCTGGGATGCAATAGAAAACCTGGGTGACTGAATCTGTAAC	1953
Qy	655	TyrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLys	674
Db	1954	TTCCTATTACACATCCAATGACATGGTCGAGGAAGACAGTGAACCTTCAGAGTTGGTGGAAA	2013
Qy	675	GluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGln	694
Db	2014	GAAGTACGCAACGAGGGTTCACGGTGACTTAAAGATAGGAATTTGGTGGCCAGACATGAAG	2073
Qy	695	ThrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHis	714
Db	2074	ACCAAAGAGGAACCTCATTCATTTCATGCACCATTATCATATGGCTTGTCTGCTATCCAT	2133
Qy	715	AlaIleValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeu	734
Db	2134	GCAGCTGTGAATTTTGGACAGTACCCCTTTTGTCTGGATACCTCCCTTAACCGTCCAACGGTG	2193
Qy	735	SerArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnPro	754

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Db      2194 AGTCGTAGTTTCATGCCGAGCAAGGTACCCAGAGTATGAGGAGCTTAAGTCAGACCCT 2253
QY      755 AspLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeu 774
Db      2254 GAATTGGCATTCTCTAAACAATCACTGCCAGTTCCAAACACTTGTTGGTGTGTCAC TG 2313
QY      775 IleGluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerPro 794
Db      2314 ATAGAAGTTCTGTCCAGGCACTCAACTGAAGAGGTTTACCTTGGGCAATGTGAGAACCCCT 2373
QY      795 GluTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSer 814
Db      2374 GAATGGACTCTAGACTGTGAGCCATTGGCAGCATTTGAGAGGTTTCAGACAGAGAAGCTGTTG 2433
QY      815 AspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGly 834
Db      2434 GAGATTGAGAACAAATATCATGGAAGGAACAAGGACAAGAGATTCAAAAACAGAAATGGG 2493
QY      835 ProValLysValProTyrThrLeuLeuPheProThrSer-----GluGly 849
Db      2494 CCGGTGAAGATGCCTTACACACTTCTCTATCCCAACACCTCAGATTATTCTAGGGAGGTT 2553
QY      850 GlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862
Db      2554 GGACTAACTGGCAAGGGAATCCCAACAGTATATCCATC 2592

RESULT 8
US-10-424-599-70317
; Sequence 70317, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 70317
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_34507C.1
US-10-424-599-70317

Alignment Scores:
Pred. No.: 0 Length: 2867
Score: 3087.50 Matches: 577
Percent Similarity: 82.20% Conservative: 125
Best Local Similarity: 67.56% Mismatches: 138
Query Match: 68.10% Indels: 14
DB: 17 Gaps: 8

US-10-731-642A-1 (1-862) x US-10-424-599-70317 (1-2867)
QY      17 LysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIle 36
Db      85 AAGAGGGTTAAAGGGAGAGTGGTTTGTATGAAGAAGGGTGTGTTGGACTTCCACGACATC 144
QY      37 AsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeu 56
Db      145 AAAGCCACGTTCTCGATCGAGTTCACGAGTTATTAGGCAAGGGTGTCTCTTCAGCTT 204
QY      57 IleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAla 76
Db      205 ATTAGTGCTACTACTCTGATCCAGCAAAAGGGTTA-----TTGAGAGGGAAGGTGGCA 258
QY      77 TyrLeuGluAsnTrpLeuThrAsnSerThrProIle---AlaAlaGlyGluSerAlaPhe 95
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Db      259 AACTTGGAGAGGTGGGTTTCGACGATTACCTCTTTGACATCAACAACACACAGAGTTC 318
QY      96 ArgValThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLys 115
Db      319 TCAGTTACGTTTGAGTGG--GATGAGAGCATGGGTGTTCTCTGGGGCATTCATAATCCGA 375
QY      116 AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis 135
Db      376 AACAATCACCATAGCCAGTTCTACCTCAAGACACTGACCATTGAAGACATTCCAGGGCAT 435
QY      136 ---GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSer 154
Db      436 GATGGTCCCTGTTAATTTTGTCTGCAATTCTTGGGTCTACCCCTGCTCATCGTTACGCCCAT 495
QY      155 AspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArg 174
Db      496 GATCGTGTCTTCTTTGCCAACCAAGGCTTATCTTCCATGTTCATACACCTGAGCCACTGCGC 555
QY      175 LysTyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGlu 194
Db      556 AAGTTCAGGGAACAAGAACTAAAACTCTCTGCGGGAAGGGTTCGGGAAGCTTAATGAG 615
QY      195 TrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGln 214
Db      616 TGGGACAGAGTCTATGACTATGCATACATACTACAATGATTGTGGACTTCCAGATGATGTCCT 675
QY      215 AspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArg 234
Db      676 GACTATGCACGCCCTGTCTTGGAGGA--TCACAATTTCCATATCCACGTAGAGGAAGA 732
QY      235 ThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMet 254
Db      733 ACTAGTCGTCCACATTGCAAAACACAGATCCTAAAACTGAGTCAAGATTGCATCTTCTA--- 789
QY      255 SerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPhe 274
Db      790 AATCTAAACGTTTATGTGCCGAGGGATGAACAGTTTGGCCATGTCAAGTTTTCAGATTTT 849
QY      275 LeuThrPheAlaLeuLysSerIleValGlnLeuLeuProGluPheLysAlaLeuPhe 294
Db      850 CTGGCATACTCACTGAAATCTGTGCTCAGGTTTGTCTTCCAGAGATTAAATCTTTGTGTGT 909
QY      295 AspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyGly 314
Db      910 GACAAAACCTAATAATGAGTTTGACACCTTTGAAGATGTACTTGATATTTATGAGGGAAGT 969
QY      315 IleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIle 334
Db      970 ATTAAGCTTCCAAGTGGACCTTTAGCGAGTAAACTGAGAGAACTTGTTCCTATGAGCTG 1029
QY      335 LeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnVal 354
Db      1030 CTGAGAGAACTTATTAGGAATGATGGTGAGAGATTCTCTCAAATTCGCGGTGCCTGATGTG 1089
QY      355 IleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAla 374
Db      1090 ATCAAAAGTGAGTAAGACTGCATGGAGCACAGATGAGGAATTTGCAAGGGAATGCTTTGCA 1149
QY      375 GlyValAsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAsp 394
Db      1150 GGGGTTAAACCTGTTATTATATCCGCGCTCTTCAGGAATTTCCCGGCGCCAGCAAGCTAGAC 1209
QY      395 ProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeu 414
Db      1210 TCCAGAGTCTATGGAGACCACAACTAGTTCATCAGAGCAACGCACATAGAAATAGTTTG 1269
QY      415 AspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHis 434
Db      1270 GATGGCTTACAATAGATGAGGCAATTCAAATATGAGGCTATTATATTAGATCATCAC 1329
QY      435 AspIleLeuMetProTyrLeuArgIleAsnThrSerThrAspThrLys-ThrTyrAl 454
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Db 1330 GACTCATTGATGCCATACATTAGTCGAATAAAC---TCTACCAACACAAAAGAACTTATGC 1386

Qy 454 aSerArgThrLeuLeuPheLeuGlnAsnGlyThrLeuLysProSerAlaIleGluLe 474

Db 1387 CTCTAGAACGCTCCTGTTTCTACAAGATGACGGTACACTCGAGCCACTGGCTATAGAGTT 1446

Qy 474 uSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAl 494

Db 1447 AAGCTTACCCCATCCACAAGGGGAACAACATGGAGCTGTGAGCAAAAGTTTTCACCTCCAGC 1506

Qy 494 aAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAs 514

Db 1507 ACAAGAAGGAGTATCGGCTTCGGTGTGGCAGCTGGCTAAGGCTTATGCAGCCGTCAATGA 1566

Qy 514 pSerGlyValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPh 534

Db 1567 TTCAGGATATCATCAATTGGTTAGCCACTGGTTATACACTCAGCAGTAATTGAACCGGTT 1626

Qy 534 eValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisPr 554

Db 1627 CATTATAGCACAAACAGGCAGTTGAGTATTCTTACCCCAATACACAAGCTCTTGAAGCC 1686

Qy 554 oHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGl 574

Db 1687 ACACCTTCAGGACACAATGCATATAAATGCCTTAGCCCGGCACACGCTCATCAATGCTGG 1746

Qy 574 yGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValVa 594

Db 1747 AGGGGTACTAGAGATTACAGTTTTCCCTGGTAAATTCGCCCTTGAAATGTGTCGCGGTTAT 1806

Qy 594 lTyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyVa 614

Db 1807 ATACAAAAGTTGGGTATTCACCGAGCAGCACTACCTGCTGATCTTCTTAAGAGGGGAAT 1866

Qy 614 lAlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTy 634

Db 1867 GGCAATTCTGATTCAAGTTCTCGTCTAGGACTAAGGCTTGATAGAGGATTATCCGTT 1926

Qy 634 rAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAs 654

Db 1927 TGCCGTGGACGCATAGAAATCTGGGATGCAATAGAAACCTGGGTGACTGAATACTGTAA 1986

Qy 654 nTyrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLy 674

Db 1987 CTTCTATTACATCCAAATGACATGGTTCAGGAAGACAGTGAACCTTCAGAGTTGGTGAA 2046

Qy 674 sGluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGl 694

Db 2047 AGAAGTACGCAACGAGGGTCACGGTGACTTAAAGATAGGAATTGGTGGCCAGACATGAA 2106

Qy 694 nThrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHi 714

Db 2107 GACCAAAAGAGAACTCATTCATTCATGCACCATATCATATGGCTTGCTTCTGCATTCCA 2166

Qy 714 sAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLe 734

Db 2167 TGCAGCTGTGAATTTTGGACAGTACCCCTTTGCTGGATACCTCCCTAACCGTCCAACGGT 2226

Qy 734 uSerArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnPr 754

Db 2227 GAGTCGTAGGTTTCATGCCGGAGCAAGGTACCCAGAGTATGAGGAGCTTAAGTCAGACCC 2286

Qy 754 oAspLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLe 774

Db 2287 TGAATTGGCATTCCTCAAAACAATCACTGCCAGTTCCAAACACTTGTGTGTGTCACT 2346

Qy 774 uIleGluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerPr 794

Db 2347 GATAGAAGTTCTGTCCAGGCACCTCAACTGAAGAGGTTTACCTTGGGCAATGTGAGAACC 2406

Qy 794 oGluTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSe 814

Db 2407 TGAATGGACTCTAGATGCTGAGCCATTGGCAGCATTTGAGAGGTTTCAGACAGAAAGCTGTT 2466

Qy 814 rAspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGl 834

Db 2467 GGAGATTGAGAACAAATATCATTGAAAGGAACAAGGACAAGAGATTCAAAAACAGAAATGG 2526

Qy 834 yProValLysValProTyrThrLeuLeuPheProThrSer-----GluGl 849

Db 2527 GCCGGTGAAGATGCCTTACACACTTCTCTATCCCAACACCTCAGATTATTCTAGGAGGG 2586

Qy 849 yGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862

Db 2587 TGGACTAACTGGCAAGGGAATCCCAACAGTATATCCATC 2626

RESULT 9

US-10-059-909-11

; Sequence 11, Application US/10059909

; Publication No. US20030074693A1

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Edgar B.

; APPLICANT: Kinney, Anthony

; APPLICANT: Klein, Theodore

; APPLICANT: Lee, Jian Ming

; APPLICANT: Pearlstein, Richard

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Shen, Jennie

; APPLICANT: Thorpe, Cathy

; APPLICANT: Tingey, Scott

; APPLICANT: Weng, Zude

; TITLE OF INVENTION: Plant Lipoxigenases

; FILE REFERENCE: BB1333 US CIP

; CURRENT APPLICATION NUMBER: US/10/059,909

; CURRENT FILING DATE: 2002-01-29

; PRIOR APPLICATION NUMBER: 09/501,422

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: 60/119,597

; PRIOR FILING DATE: 1999-02-10

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 11

; LENGTH: 2929

; TYPE: DNA

; ORGANISM: Momordica charantia

US-10-059-909-11

Alignment Scores:

Pred. No.:	1.94e-312	Length:	2929
Score:	3022.50	Matches:	554
Percent Similarity:	80.99%	Conservative:	132
Best Local Similarity:	65.41%	Mismatches:	156
Query Match:	66.66%	Indels:	5
DB:	14	Gaps:	4

US-10-731-642A-1 (1-862) x US-10-059-909-11 (1-2929)

Qy 16 GlyLysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAsp 35

Db 126 GGGAAAGAAGATCAAAGGGACGGTGGTTCTTATGAGAAGCAATGTTTGGACTTCACCCGAA 185

Qy 36 IleAsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGlu 55

Db 186 TTTTCATTCTCTCACTTCTTGACGCGCTCACTGAGCTCTTGGCGCGGGAATTTTCATTGCAA 245

Qy 56 LeuIleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAla 75

Db 246 CTTATCAGTGTCTACTCACGCT-----TCCAACGACTCGCGGAGGAAAGTTGGAAAGGGG 299

Qy 76 AlaTyrLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPhe 95

Db 300 GCGTTTCTGGAGAGGTGGCTGACTTCAGTTCGCGCACTGTTCGCTGGAGAGTCTGTGTTT 359

Qy 96 ArgValThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLys 115

Db 360 CAAGTGAACCTTTGATTGG---GAAGAGAACTTTGGATTTCAGGAGCTTTCTTCATAAAA 416

QY	116	AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis	135
Db	417	AATGGGCACACCAGTGTAGTTCTTCTCAAGTCTGTAACTCTGGAGGATGTTCTCGGCTTT	476
QY	136	GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAsp	155
Db	477	GGAAGGGTCCATTTTGACTGCAACTCATGGGTTTACCCCTCTCGAAGATACAAGAAGAT	536
QY	156	ArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLys	175
Db	537	CGCATTTTCTTGCCCAACCATACATGCCTTCCAATCGATACACCGGATTTCACITTCGTAAG	596
QY	176	TyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrp	195
Db	597	TATAGAGAGGAGGAGTGTGAACCTCAGAGGAGATGGAACAGGAGACGCTAAAGATGG	656
QY	196	AspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAsp	215
Db	657	GATAGAAATTTATGACTATGATGTTTACAACGACCTCTGTGATCCAAATGGTGGTCCCTAAC	716
QY	216	LeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThr	235
Db	717	CTTGTTCGTCTATTCTTGAGGGAGTGATCAGTACCTTACCCTCGTAGAGGGAGACA	776
QY	236	GlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSer	255
Db	777	GGAAGACCACCGCTAGAAAAGATCAAGTACGAGACGAGATTGTCGGATGTGTAGAGC	836
QY	256	LeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeu	275
Db	837	TTAAACATTTACGTACCGAGAGACGAAAATTTTCGGACACTTGAAGATGGCGGATTTCTCT	896
QY	276	ThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAsp	295
Db	897	GGGAATACGTTGAAGGTACTTTCTACATCTATCCAACGAGGACTTGAATCTATATTGAT	956
QY	296	SerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIle	315
Db	957	TCAACCCCGAGGAGATTGACAAATTCAAAGAAGTAGACGATCTCTTTGAACGAGGGTTT	1016
QY	316	LysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeu	335
Db	1017	CCCATTCCATTGAAT--ATTTTTAAGAACCTCACAGAGGACCTCGCCCCACCCCTCTTT	1073
QY	336	LysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIle	355
Db	1074	AAAGCATTTCTGAGGAGTGATGGTGAAAGATTCTCTCAAATATCCAACCTCCCAAGTTATC	1133
QY	356	GlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGly	375
Db	1134	AAAGATAACAAGTTAGGGTGGAGGACAGATGAAGAAATTTGCCAGAGAAATGATAGCGGA	1193
QY	376	ValAsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspPro	395
Db	1194	GTCAATCCTTTTGATCATTCGTCGTCTTGAAGTTTTTCCACCATTGAGTAAGTTGGACCCT	1253
QY	396	LysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAsp	415
Db	1254	CATGTTTATGGGAATCAAAACAGTACAATGACGGGAACAATAAAGCATGGTTTAGAT	1313
QY	416	GlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAsp	435
Db	1314	GGACTCACGGTTGATGAGGCAATCAAGGAAAATAAGCTCTACATATTGGATCACCATGAT	1373
QY	436	IleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSer	455
Db	1374	GCATTGATGCCATATCTTAGGAGATAAAT--TCAACATCTACAAAAACATATGCCACA	1430
QY	456	ArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSer	475
Db	1431	AGAACACTTCTCTTTTGAAGAGATGACAGTACTTTTGAAGCCATTGGCTATTGAGTTGAGC	1490

QY	476	LeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAsp	495
DB	1491	TTGCCACACCCGCAAGGAGATGAACATGGTGCCATTAGCAAACTATACTTTCCAGCTGAA	1550
QY	496	GlnGlyValGluGlySerIleTrrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSer	515
DB	1551	GGAAGAGTTGAGAGTGCCATTTGGCAACTGGCCAAAGCTTATGTAGCTGTTAATGATAGT	1610
QY	516	GlyValHisGlnLeuIleSerHisTrrpLeuAsnThrHisAlaAlaIleGluProPheVal	535
DB	1611	GGGTACCATCAACTTAACAGTCACTGGTTACACACTCATGCAGTGTGGAGCCTTTTGT	1670
QY	536	IleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHis	555
DB	1671	ATCACAACACATCGACGAGTTGAGTGTGCTCCATCCAATTTCACAAGTTTACTTGCTCCTCAT	1730
QY	556	PheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGly	575
DB	1731	TACAAAGACACCATGTTTATAAATGTCATCTGCAAGGCAAGTTTGTATTACGCGGTGGT	1790
QY	576	LeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyr	595
DB	1791	CTTATTGAATCGACTCAGTTTCCGGCAAAAGTATGCTATGGAGCTGTCTATCTTACATATAT	1850
QY	596	LysAspTrrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAla	615
DB	1851	AAGGAATGGAAGTTCCCCGATGAAGCACTCCCTACTAATCTCATTAAGAGAGGAGTAGCA	1910
QY	616	ValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAla	635
DB	1911	ATTGAGGACTCAGGCTCTCCCCATGGAGTTCGACTTCTAATAAACGATTACCCCTTTGCT	1970
QY	636	ValAspGlyLeuLysIleTrrpSerAlaIleLysSerTrrpValThrGluTyrCysAsnTyr	655
DB	1971	GTTGATGGGCTCGAGATTGGTTCAGCCATCAAAACATGGGTACAGATTACTGTCCCTC	2030
QY	656	TyrTrrpLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrrpLysGlu	675
DB	2031	TACTACAAGACGACGACGCAATTCGAAATGATGTCGAGCTCCAATCATGGTGGAAAGAA	2090
QY	676	LeuArgGluGluGlyHisGlyAspLysLysAspGluProTrrpTrrpLysMetGlnThr	695
DB	2091	CTCAGAGAAAAGTGCATACAGACAAGAAAGACGAGCCATGGTGGCCCAAAATGCAAACT	2150
QY	696	ValGlnGluLeuIleAspSerCysThrIleThrIleTrrpIleAlaSerAlaLeuHisAla	715
DB	2151	TTTTTCAGAGTTAATTGAATCATGCACCAATCATATGGATTTCTTCAGCCCTTTCACGCA	2210
QY	716	AlaValAsnPheGlyGlnTyrProTrrpAlaGlyTyrLeuProAsnArgProThrLeuSer	735
DB	2211	GCAGTCAATTTGGGCAATACCCCTTATGGAGGCTACGTTCCCAACAGACCAACCAAGC	2270
QY	736	ArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAsp	755
DB	2271	AGAAGATTTCATGCCAGAAGTAGGCACCTCGAGAGTACAAGAAGTTGAATCAAACTGAA	2330
QY	756	LysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIle	775
DB	2331	AAGGCCCTTCTAAGAACAAATCAGCTCGCAAAATAGTGGCTCTTCTTGGCCTCTCGATAATT	2390
QY	776	GluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGlu	795
DB	2391	GAAATATTGTCAAAGCACGCTTCTGACGAGGTCTACCTCGGGCAAAGAGCAGCATTTGAG	2450
QY	796	TrrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAsp	815
DB	2451	TGGACATCAGACAAATCTGCAATTGAAGCCTTTGAGAAATTTGGGAAAGAGCTGTTTGA	2510
QY	816	IleGluAspGlnIleMetGlnMetAsnValAspGluLysTrrpLysAsnArgSerGlyPro	835
DB	2511	GTTGAGGATAGAATTATCGGAAGGAATCAAGATGTGAACCTTGAGAAATCGAGCTGGCCT	2570
QY	836	ValLysValProTrrpThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGly	855

```
Db      2571  GTCAATATGCGTTACACTTTTGCTTCCATCGAGTACTGAGGGAAGCTCACTGGGAGAGGA 2630
Qy      856  ileProAsnSerValSerIle 862
Db      2631  ATTCCCAACAGTATCTCCATA 2651

RESULT 10
US-10-425-114-7612
; Sequence 7612, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7612
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700675903_FLI
US-10-425-114-7612

Alignment Scores:
Pred. No.:      2.56e-300      Length:      2782
Score:          2909.00      Matches:      549
Percent Similarity: 77.48%      Conservative: 122
Best Local Similarity: 63.39%      Mismatches:  159
Query Match:     64.16%      Indels:      36
DB:              17          Gaps:         9

US-10-731-642A-1 (1-862) x US-10-425-114-7612 (1-2782)

Qy      16  GlyLysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThr--- 34
Db      36  GGTCAATAGATAAAAGGGACAGTGGTGTGATCGCGCAAGAATGTTGGACGTGAATAGC 95
Qy      35  -----
Db      96  GTAACCAAGCGTTGGGGGAATTATTGGTCAAGGTCTCGACTTAGTTGGCTCAACACTCGAT 155
Qy      43  GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuLeSerSerValAsnAla 62
Db      156  ACTCTTACTGCCTTCTTGGCCCGATCCGTGTCTCTCCAGCTTATTAGTGCTACCAAAGCT 215
Qy      63  AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82
Db      216  GAT---GCCAACGGA--AAAGGGAAACTTGGAAAGGCTACCTTTTGGAAAGGTATCATT 269
Qy      83  ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
Db      270  ACTTCATTGCCAACTTTGGGAGCAGGCCCAATCTGCATTCAAATAATTAATTTGAATGGAT 329
Qy      103  AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122
Db      330  GATGGGAGT---GGAATTCCTGGAGCATTTATATCAAGAATTTTATGCCAACTGAGTTT 386
Qy      123  PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
Db      387  TTCCTTGTGAGTTTGACTCTTTGAAGACATTCCAAAACCATGGAAGCATCCACTTTTGTTC 446
Qy      143  AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162
Db      447  AATTCGTGGATTACAAATGCCAAACTCTTCAAAGAGTGACCGCAATTTCTTTGCCAACCCAG 506
```

```
Qy      163  AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182
Db      507  ACATATCTTCCAAGTGAGACACAGCTCCACTAGTCAAATATAGAGAAGAGATTGCAT 566
Qy      183  ThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArgValTyrAspTyrAla 202
Db      567  AATTTAAGAGGAGATGGAACGCGAAGAGTGGGAAAGGATCTATGATTATGAT 626
Qy      203  TyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGly 222
Db      627  GTCTACAATGATTAGGTGATCCGATAAAGGTAAATCATGCCCGTCTCTTCTTGA 686
Qy      223  GlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThr 242
Db      687  GGAATGACACCTTTTCCTTATCTCTGAGGGGAGAACTGGTAGAAAACCAACAGGAAA 746
Qy      243  AspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArg 262
Db      747  GATCCTAATAGTGAGAGTAGG-----AGCAATGATGTTTATCTTCCAAGA 791
Qy      263  AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIle 282
Db      792  GATCAGGCTTTTGGACACTTGAAGTCATCTGACTTTCTTACTTATGGACTAAATCCGTA 851
Qy      283  ValGlnLeuLeuProGluPheLysAlaLeuPheAsp-----SerThrHisAsnGlu 300
Db      852  TCTCAAAATGTTCTTCCATTATTGCAATCTGCTTTTGATTGAATTTTACACCCCGTGAG 911
Qy      301  PheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeuProGlnGly 320
Db      912  TTTGATAGCTTTGATGAAGTTTCATGGACTCTATTACGGCGGAATTAAGCTGCCA----- 965
Qy      321  ProLeuLeuLysAlaIleThrAspSerIle-----ProLeuGluIleLeuLys 336
Db      966  -----ACAGATATAATCAGCAAGATTAGTCCACTACCCGTTGCTTAAG 1007
Qy      337  GluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGln 356
Db      1008  GAAATCTTCCGAACCTGATGGTGAACAGGCCCTTAAAGTTTCTCTCTCTAAAGTAATTCAA 1067
Qy      357  GluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyVal 376
Db      1068  GTCAGTAAGTCTGCATGGATGACTGATGAAGAAATTTGCAAGAGAAATGCTTGTGTGTA 1127
Qy      377  AsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLys 396
Db      1128  AATCCAAACTTGATTCTGTTGTTAAAGGATTTCCCTCCAGGAAGCAAGCTAGATAGCCAA 1187
Qy      397  IleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly 416
Db      1188  GTCTATGTTGATCATACTAGTCAAAATAACCAAGAACACCTAGAGCCCAACTTAGAAGGG 1247
Qy      417  LeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIle 436
Db      1248  CTCACTGTAGATGAGGCAATTCAAAACAAGAGATTGTTCTTACTAGATCATCATGACCCA 1307
Qy      437  LeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArg 456
Db      1308  ATCATGCCATATTTGAGGCGCAATAAAT--GCAACCTCCACAAGGCTTATGCTACCAGA 1364
Qy      457  ThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeu 476
Db      1365  ACCATCCTTTTCTGAAAAATGACGGAACTTTAAGGCCACTTGCCCATAGAGTTGAGTTTG 1424
Qy      477  ProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGln 496
Db      1425  CCACATCCTCAGGGAGATCAATCTGTGCTTTTAGTCAAGTTTCTTGCCTGCAGATGAA 1484
Qy      497  GlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGly 516
Db      1485  GGTGTTGAAAGTTCTATTTGGCTGCTAGCAAAGGCTTATGTAGTTGTGAATGACTCGTGC 1544
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QY 517 ValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIle 536  
Db 1545 TATCATCAACTTGTGAGCCATTGGTTAAACACTCATGCAGTTGTTGAGCCATTCATCATA 1604  
QY 537 AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPhe 556  
Db 1605 GCAACAAACAGGCATCTCAGTGTGTTCCACCTATTTATAAACTCCTTCACCTCACTAT 1664  
QY 557 ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeu 576  
Db 1665 CGTGACACCATGAACATAAATGGCCTTGCTCGGTTATCACTGGTCAACGACGGTGGCGTT 1724  
QY 577 LeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLys 596  
Db 1725 ATAGAACAACATTTTGTGGGAAGGTATTCTGTGGAATGTCTGCTGTAGTTTACAAG 1784  
QY 597 AspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616  
Db 1785 GATTGGGTTTTTACAGATCAAGCATTCGCTGCTATATAAAAGAGGAATGGCAATT 1844  
QY 617 GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal 636  
Db 1845 GAGGATCCATCGTGCCTCATGGCATTCGCCTTGTGATAGAGGACTACCTTATGCTGTT 1904  
QY 637 AspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyr 656  
Db 1905 GATGGACTTGAGATATGGGATGCTATCAAGACATGGTCCATGAATACGTTTCTTGATC 1964  
QY 657 TyrLysSerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeu 676  
Db 1965 TACAAATCAGATGACACACTTAGAGAAGATCCTGAACTCCAAGCCTGCTGGAAGAATC 2024  
QY 677 ArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrVal 696  
Db 2025 GTAGAGTGGTGCATGGAGACAAGAAAAATGAGCCATGGTGGCTTAAGATGCAAACTCGT 2084  
QY 697 GlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAla 716  
Db 2085 GAAGAGCTAGTTGAAGCTTGGCTATCATCATATGACTGCTTCAGCACTTCATGCAGCT 2144  
QY 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736  
Db 2145 GTTAATTTTGGACAGATATCCCTATGGAGGTTTAATCTTAAACCGTCCAACTCTTAGTAGG 2204  
QY 737 AsnPheMetProGluProGlySerProGluTyrGluLeuLysThrAsnProAspLys 756  
Db 2205 CGATTTCATGCCTGAGAAAGTTCTGCTGAGTATGAGGAGCTGAGGAAGAATCCCCAGAAG 2264  
QY 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776  
Db 2265 GCTTACTTGAGACTATTACACCAAGTTTCAGACCCCTATTGACCTTTCTGTATAGAA 2324  
QY 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrp 796  
Db 2325 ATCTTGTCAGGCATGCATCTGATGAGGTGTACCTTGGGAGAGGGACAATCCAAATTGG 2384  
QY 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle 816  
Db 2385 ACATCTGATACAGAGCATTAGAGGCTTTTAAAGGTTTGGAAATAAATACTGGCACAAATT 2444  
QY 817 GluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProVal 836  
Db 2445 GAGAAATAAACTCTCAGAGAGAAACAACGATGAGAAACTGAGAAACCGTTGTGGACCAGTT 2504  
QY 837 LysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856  
Db 2505 CAAATGCCTTATACTCTGCTTTTGGCCTTCTAGTAAGGAAGGATTAACCTTCAGAGGAATT 2564  
QY 857 ProAsnSerValSerIle 862  
Db 2565 CCCAACAGTATCTCTATC 2582

RESULT 11

US-10-425-114-9323  
; Sequence 9323, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 9323  
; LENGTH: 2804  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700842448\_FLI  
US-10-425-114-9323

Alignment Scores:  
Pred. No.: 2.59e-300 Length: 2804  
Score: 2909.00 Matches: 549  
Percent Similarity: 77.48% Conservative: 122  
Best local Similarity: 63.39% Mismatches: 159  
Query Match: 64.16% Indels: 36  
DB: 17 Gaps: 9

US-10-731-642A-1 (1-862) x US-10-425-114-9323 (1-2804)

QY 16 GlyLysLysVallLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThr--- 34  
Db 58 GGTATAAGATAAAAGGACAGTGGTGTGATGCGCAAGAATGTGTGGACGTGAATAGC 117  
QY 35 -----AspIleAsnAlaSerValLeuAsp 42  
Db 118 GTAACCGCGTTGGGGAAATTATTGGTCAAGGTCTCGACTTAGTTGGCTCAACACTCGAT 177  
QY 43 GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla 62  
Db 178 ACTCTTACTGCCTTCTTGGGCCGATCCGTTCTCTCCAGCTTATTAGTGTACCAAGCT 237  
QY 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82  
Db 238 GAT---GCCAACGGA---AAAGGGAAACTTGGAAAGGCTACCTTTTGGAAAGGTATCAT 291  
QY 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102  
Db 292 ACTTCATTGCCAACTTTGGGAGCAGGCAATCTGCATTCAAAATTAATTTGAATGGGAT 351  
QY 103 AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122  
Db 352 GATGGGAGT--GGAATTCTCTGGAGCATTTTATATCAAGAATTTTATGCAAACTGAGTT 408  
QY 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142  
Db 409 TTCTCTGTGAGTTTGACTCTTTGAAGACATTCCAAACCATGGAAGCATCCACTTTGTTGC 468  
QY 143 AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162  
Db 469 AATTCGTGATTTACAATGCCAAACTCTTCAAAAGTGACCGCATTTTCTTTGCCAACCCAG 528  
QY 163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluVal 182  
Db 529 ACATATCTTCCAAGTGAGACACCAAGCTCCACTAGTCAAATATAGAGAAGAGGTTGCAT 588  
QY 183 ThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTyrAspArgValTyrAspTyrAla 202  
Db 589 AATTTAAGAGGAGATGGAACCTGGAGAACCGCAAGAGTGGGAAAGGATCTATGATTATGAT 648

QY 203 TyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGly 222  
Db 649 GTCTACAATGATTTAGGTGATCCGGATAAAGGTGAAAATCATGCCCGTCTCTTTGGA 708  
QY 223 GlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThr 242  
Db 709 GGAAATGACACCTTTCTTATCTCTCGTAGGGGAGAACTGGTAGAAAACCAACAGGAAA 768  
QY 243 AspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArg 262  
Db 769 GATCCTAATAGTGAGAGTAGG-----AGCAATGATGTTTATCTTCCAAGA 813  
QY 263 AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIle 282  
Db 814 GATGAGGCTTTGGACACTTGAAGTCATCTGACTTCTTACTTATGGACTAAATCCGTA 873  
QY 283 ValGlnLeuLeuLeuProGluPheLysAlaLeuPheAsp-----SerThrHisAsnGlu 300  
Db 874 TCTCAAAATGTTCTTCCATTATTGCAATCTGCTTTTGATTTTGAAATTCACACCCCGTGAG 933  
QY 301 PheAspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGly 320  
Db 934 TTTGATAGCTTTGATGAAGTTTCATGGACTCTATTTCAGGCGGAATTAAAGCTGCCA----- 987  
QY 321 ProLeuLeuLysAlaIleThrAspSerIle-----ProLeuGluIleLeuLys 336  
Db 988 -----ACAGATATATATACAGCAAGATTAGTCCACTACCCGTTGCTTAAG 1029  
QY 337 GluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGln 356  
Db 1030 GAAATCTTCCGAACCTGATGGTGAACAGGCCCTTAAGTTTCTCTCTTAAAGTAATTCAA 1089  
QY 357 GluAspLysThrAlaIleArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyVal 376  
Db 1090 GTGAGTAAGTTCATGGATGACTGATGAAGAATTGCAAGAGAAATGCTTGTGGTGA 1149  
QY 377 AsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLys 396  
Db 1150 AATCCAAACTTGATTCGTTGTTCTTAAGGATTTCCCTCCACGAAGCTAGATAGCCAA 1209  
QY 397 IleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly 416  
Db 1210 GTCTATGGTGATCATACTAGTCAAATAACCAAGAACACCTAGAGCCCAACTTAGAAGG 1269  
QY 417 LeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIle 436  
Db 1270 CTCACCTGTAGATGAGGCAATTCAAACACAGAGATTGTTCTACTAGATCATGACCCA 1329  
QY 437 LeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArg 456  
Db 1330 ATCATGCCATATTGAGGCGAATAAAT---GCAACCTCCACAAAGGTTATGCTACCAGA 1386  
QY 457 ThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeu 476  
Db 1387 ACCATCCTTTCTTGAAAAAATGACGGAACTTTAAGGCCACTTGGCCATAGAGTTGAGTTG 1446  
QY 477 ProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGln 496  
Db 1447 CCACATCCTCAGGAGATCAATCTGGTGCTTTTAGTCAAGTTTCTTCTGCGCTGCAGATGAA 1506  
QY 497 GlyValGluGlySerIleTyrGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGly 516  
Db 1507 GGTGTTGAAAGTTCTATTGCTGCTAGCAAGGCTTATGTAGTTGTGAATGACTCGTGC 1566  
QY 517 ValHisGlnLeuIleSerHisTyrLeuAsnThrHisAlaAlaIleGluPropheValIle 536  
Db 1567 TATCATCAACTTGTGAGCCATTGGTTAAACACTCATGCAGTTGTTGAGCCATTTCATCATA 1626  
QY 537 AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPhe 556  
Db 1627 GCAACAAACAGGCATCTCAGTGTGTTGTTCCACCTATTATATAAACTCTTCACCCTCACTAT 1686

QY 557 ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeu 576  
Db 1687 CGTGACACCATGAACATAAATGGCCTTGCTCGGTTATCATCTGCTCAACGACGGTGGCGTT 1746  
QY 577 LeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLys 596  
Db 1747 ATAGAACAAACATTTTGTGGGAAGGTATTCTGTGGAATGTCTGCTGTAGTTTACAAG 1806  
QY 597 AspTyrValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616  
Db 1807 GATTGGGTTTTTACAGATCAAGCATTCCTGCTGATCTTATAAAAAGAGGAATGGCAATT 1866  
QY 617 GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal 636  
Db 1867 GAGGATCCATCGTGCCTCATGGCATTCGCCTTGTGTATAGAGACTACCCCTTATGCTGTT 1926  
QY 637 AspGlyLeuLysIleTyrSerAlaIleLysSerTyrValThrGluTyrCysAsnTyrTyr 656  
Db 1927 GATGGACTTGAGATATGGGATGCTATCAAGACATGGGTCCATGAATACGTTTTTCTGTGAC 1986  
QY 657 TyrLysSerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTyrTyrLysGluLeu 676  
Db 1987 TACAAATCAGATGACACACTTAGAGAAGATCCTGAACTCCAAGCCTGCTGGAAAGAACTC 2046  
QY 677 ArgGluGluGlyHisGlyAspLysLysAspGluProTyrTyrProLysMetGlnThrVal 696  
Db 2047 GTAGAGGTGGTTCATGGAGACAGAAAATGAGCCATGGTGGCTTAAGATGCAAACTCGT 2106  
QY 697 GlnGluLeuIleAspSerCysThrIleThrIleTyrIleAlaSerAlaLeuHisAlaAla 716  
Db 2107 GAAGAGCTAGTTGAAGCTTGCGTATCATCATATGGACTGCTTCAGCACTTCATGCAGCT 2166  
QY 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736  
Db 2167 GTTAATTTGGACAGTATCCCTATGGAGGTTTAATCTTAAACCGTCCAACTCTTAGTAGG 2226  
QY 737 AsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLys 756  
Db 2227 CGATTTCATGCCTGAGAAAGGTTCTGCTGAGTATGAGGAGCTGAGGAAGAATCCCCAGAAG 2286  
QY 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776  
Db 2287 GCTTACTTGAAGACTATTACACCAAAAGTTTCAGACCCCTTATTGACCTTCTGTTATAGAA 2346  
QY 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyr 796  
Db 2347 ATCTTGTCAAGGCATGCATCTGATGAGGTGTACCTTGGGGAGAGGACAAATCCAAATTGG 2406  
QY 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle 816  
Db 2407 ACATCTGATACAAGAGCATTAGAGGCTTTTAAAGGTTTGGAAATAAACTGGCACAAATT 2466  
QY 817 GluAspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProVal 836  
Db 2467 GAGATAAAACTCTCAGAGAGAAAACAACGATGAGAAACTGAGAAACCGTGTGTGACCAGTT 2526  
QY 837 LysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856  
Db 2527 CAAATGCCTTATACTCTGCTTTTGCCTTCTAGTAAGGAAGGATTAACCTTTCAGAGGAATT 2586  
QY 857 ProAsnSerValSerIle 862  
Db 2587 CCCAACAGATATCTCTATC 2604

RESULT 12

US-10-425-114-6926  
; Sequence 6926, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6926
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700605994\_FLI
US-10-425-114-6926

Alignment Scores:		Pred. No.:	2.68e-300	Length:	2868
Score:			2909.00	Matches:	549
Percent Similarity:			77.48%	Conservative:	122
Best Local Similarity:			63.39%	Mismatches:	159
Query Match:			64.16%	Indels:	36
DB:			17	Gaps:	9
US-10-731-642A-1 (1-862) x US-10-425-114-6926 (1-2868)					
Qy	16	GlyLysLysValLysGlyThrValValLeuMetLysAsnValLeuAspPheThr---	34		
Db	135	GGTCATAAGATAAAGGACAGTGGTGTGATCGCGAAGAATGTGTGGACGTGAATAGC	194		
Qy	35	-----AspIleAsnAlaSerValLeuAsp	42		
Db	195	GTAACCAAGCGTTGGGGGAATTATTGGTCAAGGTCCTCGACTTAGTTGGCTCAACACTCGAT	254		
Qy	43	GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla	62		
Db	255	ACTCTTACTGCCTTCTTGGCCGATCCGTTGCTCTCCAGCTTATTAGTGTACCAAAGCT	314		
Qy	63	AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu	82		
Db	315	GAT---GCCAACGGA---AAAGGGAAACTTGGAAAGGCTACCTTTTGGAAAGGTATCAIT	368		
Qy	83	ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp	102		
Db	369	ACTTCATTGCCAACTTTGGGAGCAGGCCAATCTGCATTCAAATTAATTTGAATGGGAT	428		
Qy	103	AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe	122		
Db	429	GATGGGAGT---GGAATTCCTGGAGCATTTTATATCAAGAAATTTTATGCAAACTGAGTTT	485		
Qy	123	PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys	142		
Db	486	TTCCCTTGAGTTTGACTCTTGAAGACATTCCTCAAAGTGACCGCAATTTCTTGTCCAAACCAG	545		
Qy	143	AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln	162		
Db	546	AATTGCTGGATTACAAATGCCAAACTCTTCAAAGTGACCGCAATTTCTTGTCCAAACCAG	605		
Qy	163	AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal	182		
Db	606	ACATAATCTTCCAAGTGAGACACCAGCTCCACTAGTCAAATATAGAGAAGAAGATTGCAT	665		
Qy	183	ThrLeuArgGlyAspGlyThrGlyLysLeuGluTrpAspArgValTyrAspTyrAla	202		
Db	666	AATTTAAGAGGAGATGGAACCTGGAGAACCGCAAGAGTGGGAAAGGATCTATGATTATGAT	725		
Qy	203	TyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGly	222		
Db	726	GTCTACAAATGATTTAGGTGATCCGGATAAAGGTGAAATTCATGCCCGCTCTTCTTGGGA	785		
Qy	223	GlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThr	242		
Db	786	GGAAATGACACCTTTCCTTATCCTCGTAGGGGGAGAACTGGTAGAAAAACCAACGAGAA	845		

Qy	243	AspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArg	262
Db	846	GATCCTTAATAGTGAGAGTAGG-----AGCAATGATGTTTATCTTCCAAGA	890
Qy	263	AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIle	282
Db	891	GATGAGGCTTTTGGACACTTGAAGTCATCTGACTTCTTACTTATGAGTAAATCCGTA	950
Qy	283	ValGlnLeuLeuLeuProGluPheLysAlaLeuPheAsp-----SerThrHisAsnGlu	300
Db	951	TCTCAAAATGTTCTTCCATTATTGCAATCTGCTTTTGATTGATTTACACCCCGTGAG	1010
Qy	301	PheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeuProGlnGly	320
Db	1011	TTTGATAGCTTTGATGAAGTTCATGAGCTCTATTTCAGCGGGAATTAAGCTGCCA----	1064
Qy	321	ProLeuLeuLysAlaIleThrAspSerIle-----ProLeuGluIleLeuLys	336
Db	1065	-----ACAGATATAATCAGCAAGATTAGTCCACTACCCGTGCTTAAG	1106
Qy	337	GluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGln	356
Db	1107	GAAATCTTCCGAACACTGATGGTGAACACAGGCCCTTAAAGTTTCCTCCTCTAAAGTAATCAA	1166
Qy	357	GluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyVal	376
Db	1167	GTGAGTAAAGTCTGCATGGATGACTGATGAAGAATTTGCAAGAGAATGCTTGTGTTGTA	1226
Qy	377	AsnProValIleIleSerArgLeuGlnGluPheProLysSerLysLeuAspProLys	396
Db	1227	AATCCAAACTTGATTGTTGTTAAAGGATTTCCCTCCACGAAGCAAGCTAGATAGCCAA	1286
Qy	397	IleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly	416
Db	1287	GTCTATGTTGATCATACTAGTCAATAACCAAGAACACCTAGAGCCCAACTTAGAAGGG	1346
Qy	417	LeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIle	436
Db	1347	CTCACTGTAGATGAGGCAATTCAAACAAGAGATTGTTCCCTACTAGATCATGACCCA	1406
Qy	437	LeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArg	456
Db	1407	ATCATGCCATATTGAGGCGAATAAAT---GCAACCTCCACAAGGCTTATGCTACCAGA	1463
Qy	457	ThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeu	476
Db	1464	ACCATCCTTTCTGAAAAATGACGGAACCTTTAAGGCCACTTGCCATAGAGTTGAGTTTG	1523
Qy	477	ProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGln	496
Db	1524	CCACATCCTCAGGAGATCAATCTGCTGCTTTTAGTCAAGTTTCTGCTGCAGATGAA	1583
Qy	497	GlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGly	516
Db	1584	GGTGTGAAAGTTCTATTTGGCTGCTAGCAAGGCTTATGTAGTTGTGAATGACTCGTGC	1643
Qy	517	ValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluPropheValIle	536
Db	1644	TATCATCAACTTGTGAGCCATTGGTTAAACACTCATGCAAGTTGTTGAGCCATTTCATCA	1703
Qy	537	AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPhe	556
Db	1704	GCAACAAACAGGCATCTCAGTGTGTTTCCACCTATTATATAAACTCCTTCAACCTCAT	1763
Qy	557	ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeu	576
Db	1764	CGTGACACCATGAACATAAATGCGCTTGTCTGGTTATCACTGTTCAACGACGTTGGCGTT	1823
Qy	577	LeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValTyrLys	596
Db	1824	ATAGAAACAAACATTTTGTGGGGAAGGTATTCTGTGGAATGTCTGTGTAGTTTACAAG	1883





Db	951	TCTCAAAATGTTCTCCATTATTGCAATCTGCTTTTGATTTGAATTTTCACACCCCGTGAG	1010
QY	301	PheAspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGly	320
Db	1011	TTTGATAGCTTTGATGAAGTTTCATGGACTCTATTAGGGCGGAATTAAGCTGCCA-----	1064
QY	321	ProLeuLeuLysAlaIleThrAspSerIle-----ProLeuGluIleLeuLys	336
Db	1065	-----ACAGATATAATCAGCAAGATTAGTCCACTACCCGTGCTTAAG	1106
QY	337	GluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGln	356
Db	1107	GAAATCTTCCGAAGTGGTGAACAGGCCCTTAAGTTTCCTCCTCTAAAGTAATTCAA	1166
QY	357	GluAspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyVal	376
Db	1167	GTGAGTAAGTCTGCATGGATGACTGATGAAGAATTGCAAGAGAAATGCTTGCTGTGTA	1226
QY	377	AsnProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLys	396
Db	1227	AATCCAAACTTGATTCGTTGCTTAAGGATTTCCCTCCACGAAGCAAGCTAGATAGCCAA	1286
QY	397	IleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGly	416
Db	1287	GTCTATGGTGATCATACTAGTCAAATAACCAAGAACACCTAGAGCCCAACTTAGAAGGG	1346
QY	417	LeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIle	436
Db	1347	CTCACTGTAGATGAGGCAATTCAAAACAAGAGATGTTCTCTACTAGATCATGACCCA	1406
QY	437	LeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArg	456
Db	1407	ATCATGCCATATTGAGGCGAATAAAT--GCAACCTCCACAAAGGCTTATGCTACCAGA	1463
QY	457	ThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeu	476
Db	1464	ACCATCCTTTTCTGAAAAATGACGGAACITTAAGGCCACTTGCCCATAGAGTTGAGTTG	1523
QY	477	ProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGln	496
Db	1524	CCACATCCTCAGGGAGATCAATCTGGTGCTTTTAGTCAAGTTTTTCTGCCTGCAGATGAA	1583
QY	497	GlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGly	516
Db	1584	GGTGTGAAAGTTCTATTGGCTGTAGCAAGGCTTATGTAGTTGTGAATGACTCGTGC	1643
QY	517	ValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIle	536
Db	1644	TATCATCAACTGTGCAGCCATTGGTTAAACACTCATGCAGTTGTTGAGCCATTTCATCATA	1703
QY	537	AlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPhe	556
Db	1704	GCAACAAACAGGCATCTCAGTGTGTTCCCTTATTTATAAACTCCTTCACCCCTCACTAT	1763
QY	557	ArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeu	576
Db	1764	CGTGACACCATGAACATAAAATGGCCCTTGCTCGGTTATCACTGGTCAACGACGGTGGCGTT	1823
QY	577	LeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLys	596
Db	1824	ATAGAACAAACATTTTGTGGGAAGGATATCTGTGGAATGTCTGCTGATGTTTACAAG	1883
QY	597	AspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal	616
Db	1884	GATTGGGTTTTTACAGATCAAGCATTCGCTGCTGATCTTATAAAAAGAGGAATGGCAATT	1943
QY	617	GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal	636
Db	1944	GAGGATCCATCGTCGCCCTCATGGCATTCGCTTGATAGAGGACTACCCCTTATGCTGTT	2003
QY	637	AspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyr	656

Db	2004	GATGGACTTGAGATATGGGATGCTATCAAGACATGGGTCCATGAATACGTTTCTTGTAC	2063
QY	657	TyrLysSerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeu	676
Db	2064	TACAAATCAGATGACACACTTAGAGAGAGATCCTGAACTCCAAGCCTGCTGGAAGAACTC	2123
QY	677	ArgGluGluGlyHisGlyAspLysAspGlyProTyrTrpProLysMetGlnThrVal	696
Db	2124	GTAGAGGTGGTTCATGGAGACAAGAAAATGAGCCATGGTGGCCTAAGATGCAAACTCGT	2183
QY	697	GlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAla	716
Db	2184	GAAGAGCTAGTTGAAGCTTGGCTATCATCATATGGACTGCTTCAGCACTTCATGCAGCT	2243
QY	717	ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg	736
Db	2244	GTTAATTTTGGACAGTATCCCTATGGAGGTTTAATCTTAAACCCGTCCAACTCTTAGTAGG	2303
QY	737	AsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLys	756
Db	2304	CGATTTCATGCTGAGAAAGGTTCTGCTGAGTATGAGGAGCTGAGGAAGAATCCCAGAAG	2363
QY	757	ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu	776
Db	2364	GCTTACTTGAAGACTATTACACCACAAAGTTTCAGACCCCTTATTGACCTTTCTGTATAGAA	2423
QY	777	IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrp	796
Db	2424	ATCTTGTCAAGGCATGCATCTGATGAGGTGTACCTTGGGGAGAGGACAAATCCAAATTGG	2483
QY	797	ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle	816
Db	2484	ACATCTGATACAAGAGCATTAGAGGCTTTTAAAGGTTTGGAAATAAACTGGCACAAATT	2543
QY	817	GluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProVal	836
Db	2544	GAGAATAAACTCTCAGAGAGAAACAACGATGAGAAACTGAGAAACCGTTGTGGACCAGTT	2603
QY	837	LysValProTyrThrLeuLeuPheProThrSerGluGlyLeuThrGlyLysGlyIle	856
Db	2604	CAAAATGCCTTATACTCTGCTTTTGCCTTCTAGTAGGAAGGATTAACTTTCAGAGGAATT	2663
QY	857	ProAsnSerValSerIle 862	
Db	2664	CCCAACAGATATCTCTATC 2681	
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; Sequence 8087, Application US/10425114			
; Publication No. US20040034888A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Jingdong			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Screen, Steven E			
; APPLICANT: Tabaska, Jack E			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; FILE REFERENCE: 38-21(53313)B			
; CURRENT APPLICATION NUMBER: US/10/425,114			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 73128			
; SEQ ID NO 8087			
; LENGTH: 2704			
; TYPE: DNA			
; ORGANISM: Glycine max			
; FEATURE:			
; OTHER INFORMATION: Clone ID: 700733503_FLI			
US-10-425-114-8087			
Alignment Scores: 5.76e-294 Length: 2704			
Pred. No.:			

Score:	2849.50	Matches:	535
Percent Similarity:	77.02%	Conservative:	122
Best Local Similarity:	62.72%	Mismatches:	155
Query Match:	62.85%	Indels:	41
DB:	17	Gaps:	9
US-10-731-642A-1 (1-862) x US-10-425-114-8087 (1-2704)			
Qy	16	GlyLysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAsp	35
Db	51	GGTCATAAGATAAAAGGGACAGTGGTGTGATCGCGCAAGATGTGTTGGACGTGAATAGC	110
Qy	36	IleAsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGlu	55
Db	111	GTAACCAGC-----GTTGGGGGAATTATT-----	134
Qy	56	LeuIleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAla	75
Db	135	-----GGTCAAGCCCAACGGA---AAAGGGAAACTTTGGAAAGGCT	170
Qy	76	AlaTyrLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPhe	95
Db	171	ACCTTTTGGGAAGGTATCATTTACTTTCATTTGCCAACTTTGGGAGCAGGCCAATCTGCAITTC	230
Qy	96	ArgValThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLys	115
Db	231	AAAATTAAATTTGAATGGGATGATGGGAGT---GGAATTCTCGAGCATTTTATATCAAG	287
Qy	116	AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis	135
Db	288	AATTTTATGCCAAACTGAGTTTTTCTTGTGAGTTTGAATCTTGAAGACATTTCCAAACCAT	347
Qy	136	GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAsp	155
Db	348	GGAAGCATCCACTTTGTTTGCAATTCTGTGGATTTACAATGCCAAACTCTTCAAAAGTGAC	407
Qy	156	ArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLys	175
Db	408	CGCATTTTCTTGGCAACCAGACATATCTTCCAAGTGAGACACCAGCTCCACTAGTCAAA	467
Qy	176	TyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluTrp	195
Db	468	TATAGAGAAGAAGAGTTGCATAATTTAAGAGGAGATGGAACCTGAGAGACGCAAGAGTGG	527
Qy	196	AspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAsp	215
Db	528	GAAAGGATCTATGATTATGATGTCTACAATGATTTAGGTGATCGGATAAAGGTGAAAT	587
Qy	216	LeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThr	235
Db	588	CATGCCCGTCCTGTTCTTGGAGGAATGACACCTTTCTTATCTCGTAGGGGAGAACT	647
Qy	236	GlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSer	255
Db	648	GGTAGAAAACCAACAAGGAAGATCCTTAATAGTGAGAGTAGG-----AGC	692
Qy	256	LeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeu	275
Db	693	AATGATGTTTATCTTCCAAGAGATGAGGCTTTTGGACACTTGAAGTCATCTGACTTTCIT	752
Qy	276	ThrPheAlaLeuLysSerIleValGlnLeuLeuProGluPheLysAlaLeuPheAsp	295
Db	753	ACTTATGGACTAAATCCGTATCTCAAAATGTTCTTCCATTATTGCAATCTGCTTTTGAT	812
Qy	296	-----SerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGly	313
Db	813	TTGAATTTCAACCCCGTGAGTTTGATAGCTTTTGATGAAGTTTCATGGACTCTATTTCAGGC	872
Qy	314	GlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIle-----	330
Db	873	GGAATTAAGCTGCCA-----ACAGATATAATCAGCAAGATT	908
Qy	331	---ProLeuGluIleLeuLysGluLeuArgSerAspGlyGluGlyLeuPheLysTyr	349

Db	909	AGTCCACTACCCGTCGTTAAGGAAATCTTCCGAACTGATGGTGAACAGGCCCTTAAGTTT	968
Qy	350	ProThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGly	369
Db	969	CCTCCTCTAAAGTAATTCAAGTGAGTAAGTCTGCATGGATGACTGATGAAGAATTTGCA	1028
Qy	370	ArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGlnGluPheProPro	389
Db	1029	AGAGAAATGCTTGTGTTGTTAAATCCAAACTTGATTGTCGTTGTCTTAAGGAGTTCCCTCCA	1088
Qy	390	LysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGln	409
Db	1089	CGAAGCAAGCTAGATAGCCCAAGTCTATGGTGATCATACTAGTCAAAATAACCAAGAACAC	1148
Qy	410	IleGluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPhe	429
Db	1149	CTAGAGCCCAACTTAGAAGGGCTCACTGTAGATGAGGCAATTCAAAACAAGAGATTGTTTC	1208
Qy	430	IleLeuAsnHisHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAsp	449
Db	1209	CTACTAGATCATCATGACCCCAATCATGCCATATTTGAGCGCAATAAAT---GCAACCTCC	1265
Qy	450	ThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysPro	469
Db	1266	ACAAAGGCTTATGCTACCAGAACCATCCTTTTCTGAAAAAATGACGGAACCTTTAAGACCA	1325
Qy	470	SerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLys	489
Db	1326	CTTGCCATAGAGTTGAGTTTGCCACATCCTCAGGGAGATCAATCTGGTGCTTTTAGTCAA	1385
Qy	490	ValTyrThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyr	509
Db	1386	GTTTTCCTGCTGCAGATGAAGGTGTTGAAAGTTCTATTGGCTGTAGCAAAAGGCTTAT	1445
Qy	510	AlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeuAsnThrHisAla	529
Db	1446	GTAGTTGTGAATGACTCGTGCTATCATCAACTTGTGAGCCATTTGTTAAACACTCATGCA	1505
Qy	530	AlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyr	549
Db	1506	GTTGTTGAGCCATTTCATCATAGCAACAACAGGCATCTCAGTGTGTTCCACCCTATTAT	1565
Qy	550	LysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIle	569
Db	1566	AAACTCCTTCACCCTCACTATCGTGACACCATGAACATAAATGGCCTTGCTCGGTTATCA	1625
Qy	570	LeuIleAsnGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGlu	589
Db	1626	CTGTCACACGACGGTGGCGTTATAGAAACAACATTTTTTGTGGGGAAGGTATTCTGTGGAA	1685
Qy	590	MetSerAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeu	609
Db	1686	ATGTCGCTGTAGTTTACAAGGATTGGGTTTTTACAGATCAAGCATTCCTGCTGATCTT	1745
Qy	610	IleLysArgGlyValAlaValGluAspSerSerSerProLeuGlyIleArgLeuLeuIle	629
Db	1746	ATAAAAAGAGGAATGGCAATTGAGGATCCATCGTGCCTCATGGCATTCGCCTTGTGATA	1805
Qy	630	GlnAspTyrProTyrAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpVal	649
Db	1806	GAGGACTACCTTATGCTGTTGATGGACTTGAGATATGGGATGCTATCAAGACATGGGTC	1865
Qy	650	ThrGluTyrCysAsnTyrTyrLysSerAspAlaValGlnLysAspThrGluLeu	669
Db	1866	CATGAATACGTTTCTTGTTACTACAAATCAGATGACACACTTAGAGAAGATCCTGAACCTC	1925
Qy	670	GlnAlaTrpTrpLysGluLeuArgGluGlyHisGlyAspLysLysAspGluProTrp	689
Db	1926	CAAGCTGCTGGAAAGAACTCGTAGAGGTGGGTTCATGGAGACAAGAAAAATGAGCCATGG	1985
Qy	690	TrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIle	709







GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 14, 2005, 04:35:30 ; Search time 6629 Seconds  
(without alignments)  
4949.676 Million cell updates/sec

Title: US-10-731-642A-1  
Perfect score: 4534  
Sequence: 1 MFLEKIVDAITGKDDGKKV.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10731642/runat\_10032005\_102236\_5470/app\_query.fasta\_1.1031  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10731642 @CGN\_1\_1\_3848@runat\_10032005\_102236\_5470 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2696.5	59.5	3135	3 AY103567	AY103567 Zea mays
2	2624	57.9	2571	9 CL962567	CL962567 OsIFCC008
3	1874	41.3	2682	9 CL969033	CL969033 OsIFCC017
4	1771	39.1	2857	3 CNS0AAKP	BX816626 Arabidops
5	1743.5	38.5	2928	3 AY110012	AY110012 Zea mays
6	1717.5	37.9	2739	3 AY109573	AY109573 Zea mays
7	1658	36.6	4458	9 CL975314	CL975314 OsIFCC027
8	1509.5	33.3	918	7 CK268592	CK268592 EST714670
9	1462.5	32.3	2643	9 CL979503	CL979503 OsIFCC033

10	1403.5	31.0	2835	9	CL979507	CL979507 OsIFCC033
11	1277.5	28.2	916	7	CK271202	CK271202 EST717280
12	1262	27.8	935	7	CK255133	CK255133 EST738770
13	1259.5	27.8	910	7	CV471979	CV471979 45239.1 C
14	1235.5	27.2	983	7	CV472045	CV472045 45315.1 C
15	1233	27.2	1473	3	CNS0AAZ0	BX818403 Arabidops
16	1198	26.4	765	4	BI422183	BI422183 EST532849
17	1189	26.2	882	7	CV471573	CV471573 44757.1 C
18	1188.5	26.2	808	4	BM411588	BM411588 EST585915
19	1186.5	26.2	893	7	CV470308	CV470308 43145.1 C
20	1184	26.1	782	7	CO100713	CO100713 GR_Eb002
21	1182.5	26.1	830	7	CV472049	CV472049 45319.1 C
22	1181	26.0	790	7	CV469947	CV469947 42715.1 C
23	1176	25.9	722	2	AW030773	AW030773 EST274028
24	1170.5	25.8	868	7	CO129962	CO129962 GR_Eb31H
25	1158	25.5	1091	3	CNS0AB1Z	BX818359 Arabidops
26	1156.5	25.5	806	7	CV472057	CV472057 45329.1 C
27	1149.5	25.4	801	7	CV472255	CV472255 45564.1 C
28	1149.5	25.4	845	7	CO117469	CO117469 GR_Eb01E
29	1138.5	25.1	755	4	BI422298	BI422298 EST532964
30	1133.5	25.0	764	7	CV470601	CV470601 43502.1 C
31	1131	24.9	895	7	CK250792	CK250792 EST734429
32	1127	24.9	771	4	BG888415	BG888415 EST514266
33	1123.5	24.8	775	4	BM412715	BM412715 EST587053
34	1122	24.7	663	4	BG890287	BG890287 EST516138
35	1115	24.6	741	5	BQ987346	BQ987346 QGF11P12.
36	1114	24.6	798	7	CO113220	CO113220 GR_Eb013
37	1113	24.5	791	4	BM411405	BM411405 EST585732
38	1112.5	24.5	752	4	BG593074	BG593074 EST491752
39	1111.5	24.5	728	4	BI423111	BI423111 EST533777
40	1108	24.4	1158	7	CK161284	CK161284 FGAS01385
41	1104.5	24.4	749	4	BM411164	BM411164 EST585491
42	1103	24.3	880	7	CV472589	CV472589 45955.1 C
43	1102	24.3	817	4	BM411179	BM411179 EST585506
44	1102	24.3	841	7	CV470085	CV470085 42879.1 C
45	1101	24.3	774	7	CV471624	CV471624 44818.1 C

ALIGNMENTS

RESULT 1	AY103567	3135 bp	mRNA	linear	HTC 16-OCT-2002
AY103567	AY103567	PCO116252	mRNA sequence.		
LOCUS	Zea mays				
DEFINITION	AY103567				
ACCESSION	AY103567				
VERSION	AY103567.1	GI:21206645			
KEYWORDS	HTC.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	1 (bases 1 to 3135)				
AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.				
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2 (bases 1 to 3135)				
AUTHORS	Coe,E.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.				
FEATURES	Location/Qualifiers				
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	/organism="Zea mays"				



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/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

Alignment Scores:
Pred. No.:      6.28e-282      Length:      3135
Score:          2696.50      Matches:      533
Percent Similarity: 72.31%      Conservative: 112
Best Local Similarity: 59.75%      Mismatches:  214
Query Match:     59.47%      Indels:      33
DB:              3              Gaps:       11

US-10-731-642A-1 (1-862) x AY103567 (1-3135)

QY      1  MetPheLeuGluLysIleValAspAlaIleThrGlyLysAsp-----Asp 15
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Db      235  ATGTTCTGGCACGGGTTCGCGGACCGGCTGACGGGAAGAACAGGAGGCGTGGAGCGAG 294

QY      16  GlyLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAsp 35
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db      295  GGC---AAGATCCGGGCACGGTGGGTCAAGAGGAGGTGCTGGACGTCGGCGGAC 351

QY      36  IleAsnAlaSerValLeuAspGlyValLeuGluPheLeuGly-----ArgArgValSer 53
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db      352  TTCAACGCTCGCTCCTCGACGGCTCCACAGGATCCTCGGCTGGGACGACGGCGTCGCC 411

QY      54  LeuGluLeuIleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSer 73
      ::::  |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db      412  TTCAGCTCGTCAGCGCCACCGCGGCCGACCCACAGCAACGGGGCGCTGGCAAGTGGGG 471

QY      74  LysAlaAlaTyrLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSer 93
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db      472  AAGCGCGGCACCTGGAGGAGCGGTGTGTCGTCGAAGTCCACGGCGGACGGGAGACC 531

QY      94  AlaPheArgValThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIle 113
      ::::  |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db      532  GTGTACCGGTGAGCTTCGAGTGGGACGAGTCGCAG---GGCATCCCGGGCGCGTCTC 588

QY     114  IleLysAsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValPro 133
      ::::  |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db      589  GTCAGGAACCTGCAGCACGCCGAGTTCTTCTCAAGACGCTCACCTCGAGGGCGTCCCA 648

QY     134  AsnHisGlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLys 153
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Db      649  GGCAAGGGCACCGTCTCTTCGTCGCCAACTCGTGGGTCTACCCGCAAAATGCCGGCG 708

QY     154  SerAspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeu 173
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Db      709  CAGGAACGCATCTTCTTCGCCAACGCACACCTATCTGCCGAGCAAAATGCCGGCGGT 768

QY     174  ArgLysTyrArgGluAsnGluLeuValThrLeuArgGly---AspGlyThrGlyLysLeu 192
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Db      769  GTGCCTTATCGGCAAGATGAGCTCAAGATCTCCGTGGCGACGATAATCCTGGACCATA 828

QY     193  GluGluTrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLys 212
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Db      829  CAGGAGCATGATCGCGTCTACCGTTACGACTACTACAATGACCTTGTGTGATCCCGACA 888

QY     213  GlyGlnAspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArg 232
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Db      889  GGCGAAGAGCAGCGCTCGGCCGATCCTCGGTGGCAGCCCAAGAACACCCGTATCCCGTC 948

QY     233  GlyArgThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeu 252
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```

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Db      949  TGCAGAACTGGCCGGCACCCCAACAAAGAAAGACCACAAATTCGAGAGCAGGCTT---TTC 1005

QY     253  LeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSer 272
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Db     1006  CTGCTGAACCTGAACATCTACGTCCCGCGTGACGACGCTTGGGCATCTCAAGATGTCG 1065

QY     273  AspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuProGluPheLysAla 292
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1066  GACTTCCTTGGGTACTCGCTGAAGACGATCATCGAGCTGTCTTCCAACACTGGGGACT 1125

QY     293  LeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGlu 312
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1126  TTCGTGATGACACGCCCAAGGAGTTCGATTTCGTTGAGGATATCCTCGGGCTCTACGAG 1185

QY     313  GlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeu 332
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1186  CTGGGCCCAGAGGCCCAACAAACCCACTGATAGCAGAGATCAGGAAGAAGATCCCCAGC 1245

QY     333  GluIleLeuLysGluLeuLeu---ArgSerAspGlyGluGlyLeuPheLysTyrProThr 351
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1246  GAGTTCCTTCGAAGCATTCCTGCCGAACGGTAGCCATGACCACCCGCTAAAGATGCCCTT 1305

QY     352  ProGlnValIleGlnGluAsp-----LysThrAlaTrpAr 363
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1306  CCAATGTCTCAATCAATCAGATGTGTGAAAAAGGCTCCGGGAGTTTAAGTTTGGCTGGAG 1365

QY     363  qThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerAr 383
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1366  GACTGACGAAGAGTTCGCGAGAGAGACACTTGCAGGCGTGAACCCAGTAATCATCAACG 1425

QY     383  gLeuGlnGluPheProProlysSerLysLeuAspProlysIleTyrGlyAsnGlnAsnSe 403
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1426  TCTGGAGGAGTTCGCCGCTAAAGCACCTTGGACCCCAAGGCAGTACGGAGACCACACAG 1485

QY     403  rThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGluAlaI 423
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1486  CAAGATCACTGAAGTCAATCCGCGCATAAACATGCGGAGGCTGTCCGTGCAGAACGCACT 1545

QY     423  eLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyrLeuArgAr 443
      ::::  |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1546  GAGGAACAAGAGGCTCTTCATCCTAGACCACCATGACCATTTTCATGCCGTACCTCGACA 1605

QY     443  gIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAs 463
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
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QY     463  pAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGl 483
      ::::  |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1666  CGATGGCACGCTGAAGCCCCCTGGCCATCGAGCTGAGCCCTGCCCCACCCTGACGGCCAGCA 1725

QY     483  nPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySerIleTr 503
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Db     1726  GCGCGCGCGGTCAAGCAAGGTGTACACCCCGCTCACACCGGCGTCGAGGGCCACGCTCTG 1785

QY     503  pGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHi 523
      |||||  ::::  |||||  ::::  |||||  ::::  |||||  ::::
Db     1786  GCAGTCGCCAAGGCTTATGCTGCGTAAACGACTCTGCCCTGGCATCAGCTGATCAGCCA 1845

QY     523  sTrpLeuAsnThrHisAlaAlaIleGluPropheValIleAlaThrAsnArgGlnLeuSe 543
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Db     1846  CTGGCTGAACACGCAACGCGGTGATCGAGCCGTTTCGTAATCGCGCAAAACCGGCAGCTCAG 1905

QY     543  rAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAs 563
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Db     1906  CGTGGTGCATCCCGTGCACACAGCTGCTGAGCCCCGCACTACCGTGACACGCTGAACATCAA 1965

QY     563  nAlaLeu-AlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrValPheP 583
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QY     583  roAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPheProGluG 603
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Db 613 GTCTAACAGCACTCGGCTCCCCGACTCCGGCAAC-----CCTGCCCCATCCTCGGC 666  
QY 223 GlySerSerGluTyrProTyrProArgGlyArgThrGlyArgLysProThrLysThr 242  
Db 667 GGCTCCCCGACACCCCTACCTCGCCGCGCCGACACCGGCCGCAACCCACCACC 726  
QY 243 AspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArg 262  
Db 727 GATCCGGACTCGGAGAGTAGGCTGTGCTGGTGGAG-----CAGATCTACGTGCCGCG 780  
QY 263 AspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIle 282  
Db 781 GACGAGCGGTTCGGGCACCTGAAGATGGCGGACTTCCTGGGCTACTCGATCAAGGCGATC 840  
QY 283 ValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAsp 302  
Db 841 GCGGAGGGGATCGTCCGGCGATCCGCACGTACGTGGACACCCACCCCGCGGATTCGAC 900  
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QY 383 ArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsn 402  
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QY 403 SerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGluAla 422  
Db 1201 AGCAGCATACGCGGCGCACATCGGGAGCAACCTCGAGGGCCTCACCGTGCAGAGCG 1260  
QY 423 IleLysThrAsnArgLeuPheIleLeuAsnHisAspIleLeuMetProTyrLeuArg 442  
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QY 623 LeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTyr 642  
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QY 683 AspLysLysAspGluProTyrTrpProLysMetGlnThrValGlnGluLeuIleAspSer 702  
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QY 723 ProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGluPro 742  
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Db 2164 GGGACGGAGCGGTACGCGGAGTGGGGCGGACCCCGGAGCGGCGCTTCATCCGACCATC 2223  
QY 763 ThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHisSer 782  
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QY 802 oLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMetG1 822  
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QY 822 nMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThrLe 842  
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QY 842 uLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGlyI1 856  
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QY 856 eProAsnSerValSerIle 862  
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RESULT 3

CL969033  
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DEFINITION OsIFCC017680 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL969033  
VERSION CL969033.1 GI:52392695  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2682)

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

Unpublished (2004)

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Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80481559

Fax: 86-10-80488676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

Location/Qualifiers

1. 2682

/organism="Oryza sativa (indica cultivar-group)"

/mol\_type="genomic DNA"

/db\_xref="taxon:39946"

/clone\_lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Alignment Scores:

Pred. No.:	2.64e-192	Length:	2682
Score:	1874.00	Matches:	384
Percent Similarity:	60.33%	Conservative:	127
Best Local Similarity:	45.34%	Mismatches:	310
Query Match:	41.33%	Indels:	26
DB:	9	Gaps:	12

US-10-731-642A-1 (1-862) x CL969033 (1-2682)

QY 20 LysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSer 39

DB 205 AGGGCCGTGTGACCGTGCGGGCGGAGGGCGCAAGGAGGACGCCAAGGACCGATTCCGCCGAG 264

QY 40 ValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSer 59

DB 265 CAGCTCGACGCCCTCGCCGACAGGGTCGGCGCGCAGCGTCCTCCTCGAGCTCGTCAGCACG 324

QY 60 ValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGlu 79

DB 325 ---GAGACCGACCCCAAGGAAGGGACGCCG---AAGAAGAGCAAGCCGTCGGCGCTGGTG 378

QY 80 AsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPhe 99

DB 379 GGGTGGTTCGACAAGAAG-----GACGTCAAGCGCGAGCGGTGGTGATC 423

QY 100 AspTrpAsp-----AspGluGluPheGlyValProGlyAlaPheIleIleLysAsn 116

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QY 137 LysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArg 156

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QY 157 IlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyr 176

DB 601 GTGTTCTTCAGCAACCGCCGTACCTGCCGTGGAGACGCCCGCGGGGCTGAGGGAGCTC 660

QY 177 ArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluTyrPasp 196

DB 661 CGGCTCCGGGAGCTCGCCGACCTCCGCGGCGACGCCACCGCGGAGCGGAGGATCACCGAC 720

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QY 237 ArgLysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeu 256

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Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
AUTHORS 1 (bases 1 to 2857)  
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,  
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,  
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome  
Annotation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2857)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli  
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,  
Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis  
genome released by MIPS (Munich Information center for Protein  
Sequences). 5 prime and 3 prime are assembled with Phrap.  
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QY	378	ProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIle	397
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QY	416	GlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAsp	435
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QY	454	AlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGlu	473
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QY	554	ProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGly	573
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QY	574	GlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaVal	593
DB	1892	GGAGGAATCATCGAAAGTTGCTTCTACTCCCGAATAATACGCAATGGAAGCTTACTCTGCA	1951
QY	594	ValTyrLysAsp--TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArg	612
DB	1952	CGGTACAGAGCATGTGGCGATTGACATGGAAGGACTTCTCTGCTGATCTGTGTCGGAGG	2011
QY	613	GlyValAlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyr	632
DB	2012	GGAATGGCAGAAAGGATTTCATCAGCCGAATGTGGCGTGAGGCTTGTGATTGACGATTAT	2071
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QY	653	CysAsnTyrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrp	672
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DB	2192	TGGGATGAGATCAAGAACAAGGTCTATTACGACAAGAAAGACGAGCCTTGGTGGCCTAAA	2251
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Db 2339 CTGTCGACGCACTNNNNNGACGAGGAGTACCTCGCGGAGGCGCGGACGCGGCGTGACG 2398  
QY 798 LysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGlu 817  
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QY 818 AspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProValLys 837  
Db 2459 GAAGCCATCGATAGTCGAACCGGACCGGACGAGGAGGAANNNGTCCGCGCCCGGGTG 2518  
QY 838 ValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIlePro 857  
Db 2519 CTNCCGTACGAGTGTGCGGCCAGCTGCGCGCCNNNNNTACGTCGCGCGGCGTGCCT 2578  
QY 858 AsnSerValSerIle 862  
Db 2579 AACAGCATCTCCATA 2593

RESULT 7  
LOCUS CL975314 4458 bp DNA linear GSS 21-SEP-2004  
DEFINITION OsIFCC027243 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL975314  
VERSION CL975314.1 GI:52405149  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 4458)  
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.  
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis  
JOURNAL Unpublished (2004)  
COMMENT Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
FEATURES  
Location/Qualifiers  
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Percent Similarity: 57.55% Conservative: 143  
Best Local Similarity: 41.06% Mismatches: 268  
Query Match: 36.57% Indels: 100  
DB: 9 Gaps: 18  
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QY 61 AsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsn 80  
Db 2062 -----AGCTCCGTCCGCTACGACAAGCTC 2085  
QY 81 TrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAsp 100  
Db 2086 TGG-----CGCTTCGAC 2097  
QY 101 TrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeu----- 117  
Db 2098 ACGGAG-----GCGCTCCCGCCGACCTCGTCCGCGCGCATGGCCGAGGAG 2145  
QY 118 ---HisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGly 136  
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QY 137 LysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArg 156  
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QY 157 IlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyr 176  
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QY 197 ArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeu 216  
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QY 217 SerArgProValLeuGlyGlySerSerGluTyrProTyrProTyrProTyrArgGlyArgThrGly 236  
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Db 2587 AAGACGGTGGGTGGTGGTCTCCAGCGCGCGCTGCGCGGCGGCGAGTCGCTCTCTCGAC 2646  
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Qy 357 -----GluAspLysThrAla 361  
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Db 4435 ATCCCAACAGCACATCCATC 4455

RESULT 8  
CK268592 918 bp mRNA linear EST 03-AUG-2004  
LOCUS EST714670 potato abiotic stress cdna library Solanum tuberosum cDNA  
DEFINITION clone POACH67 5' end, mRNA sequence.  
ACCESSION CK268592  
VERSION CK268592.1 GI:39825570  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 918)  
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.  
TITLE Generation of ESTs from abiotic stressed potato tissue  
JOURNAL Unpublished (2003)  
COMMENT Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via http://genome.arizona.edu/orders/.  
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES  
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/organism="Solanum tuberosum"  
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/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="POACH67"

/tissue\_type="abiotic stress treated leaf and root tissue"  
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/clone\_lib="potato abiotic stress cdna library"  
/note="Vector: pCMVSPORT6.1; Site\_1: EcoRI; Site\_2: NotI;  
supplier: Solanum tuberosum var. Kennebec plants were  
grown from cuttings on a 16hr light/8 hr dark cycle at 25  
C for 3-4 weeks. Abiotic stress conditions were applied to  
four separate sets of plants. Set 1 involved saturation of  
the soil with 150 mM NaCl and tissues were harvested at  
following application of the salt stress (leaves: 2hr,  
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
Set 2 were grown under the standard conditions and then  
were water stressed by withdrawal of further watering  
applications. Drought stressed plants were harvested after  
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
and 5d). Set 3 were grown under the standard conditions  
and then were cold stressed by placement at 4 C. Cold  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
and 2d. Set 4 were grown under the standard conditions and  
then were heat stressed by placement at 35 C. Heat  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d and 4d and heat-stressed roots were harvested at 6 hr,  
12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
equal RNA from each tissue and stress was pooled to  
construct the cdna library. RNA sample."

## ORIGIN

Alignment Scores:		
Pred. No.:	2.65e-153	918
Score:	1509.50	281
Percent Similarity:	96.05%	Conservative: 11
Best Local Similarity:	92.43%	Mismatches: 11
Query Match:	33.29%	Indels: 1
DB:	7	Gaps: 1

US-10-731-642A-1 (1-862) x CK268592 (1-918)

545	Qy	LeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAla	564
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6	Db	GTTCAACCCTATTTCATAAGCTTCTCCTTCCTCATTTTCGTGAACGATGAACATAAAATGCT	65
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66	Db	TTAGCAAGACAAATCCTAATCAATGGTGGCGGACTTCTTGAAATTTACCGTCTTCCCTGCC	125
585	Qy	LysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPheProGluGlnAla	604
		:::     :::     :::	
126	Db	AAATATTCCATGGAACTGTCAATCAGTAATTTACAAAGACTGGATTTTCCGGAACAAGCA	185
605	Qy	LeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSerProLeuGly	624
186	Db	CTTCCTGCTGATCTCATCAAAAGGGAGTGGCTGTTGAGGACTCAAGCTCCCCACATGGC	245
625	Qy	IleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTrpSerAla	644
246	Db	ATTGCGTTACTGATTCAGGACTATCCATATGCTGTTGATGGGTGGAAATTTGGTCAGCA	305
645	Qy	IleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAlaValGln	664
306	Db	ATCAAAAGTTGGGTAAACAGAATAATTGCAACTACTATTACAAATCAGATGACGCGGTACAG	365
665	Qy	LysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHisGlyAspLys	684
366	Db	AAAGACACTGAACCTCCAAGCCTGGTGAAGGAGCTCCGTGAAGAAGGACATGGCGACAAG	425
685	Qy	LysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThr	704
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Db 2401 ATGGGCACGCACGCGAGTCAGCGTGGATGGCGACAGGAGGTGAGGGCGGTCGGG 2460

Qy 808 ArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGlu 827

Db 2461 AGGTTCAACGAGAGGATGATGATCGCGGAGATGATCGACTGCCGGAACAAGGATCCG 2520

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Db 2521 GAGCGAAAGAACCGCAGGGCCCGCGGTGGTGGCTACGTGCTCAAGCGCTCCTAC 2580

Qy 847 -----SerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862

Db 2581 GGTGACCCTAAGACATGACGTCCGTGATGGAGATGGGTATCCCCAACAGCATCTCAATT 2640

RESULT 10

CL979507

LOCUS

DEFINITION

OSIFCC033431 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .2835

/organism="Oryza sativa (indica cultivar-group)"

/mol\_type="genomic DNA"

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/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Alignment Scores:

Pred. No.: 6.2e-141 Length: 2835

Score: 1403.50 Matches: 323

Percent Similarity: 54.14% Conservative: 115

Best Local Similarity: 39.93% Mismatches: 274

Query Match: 30.96% Indels: 97

DB: 9 Gaps: 22

US-10-731-642A-1 (1-862) x CL979507 (1-2835)

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Db 610 ACATCCTCAGGTCCATTAGCGCGGACGAAGAAGAAATTCCTCCGCAFAAAGGCAGCTGAT 669

Qy 92 GluSerAlaPheArgValThrPheAspTrpAspAspGluGluPheGlyValProGlyAla 111

Db 670 GACTCTCGTCCCTCTATCTTACTCAAATGGTGGGACGAGAACTCTCAAGTTTCCGGCATC 729

Qy 112 PheIleIleLysAsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAsp 131

Db 730 GTCATAAATCGCCAAAAGAGATGAGGAAGTGTGCCAGCTGAAGAAAGTACTT----- 783

Qy 132 ValProAsnHisGlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLys 151

Db 784 -----GGAGAAGCTACTCGCATTTGTGAATTCTG----- 810

Qy 152 TyrLysSerAspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAsp 171

Db 811 -----TACCTCCCGTCTCAGACGCCGAGG 834

Qy 172 ThrLeuArgLysTyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLys 191

Db 835 GGCGTGAAGATCTCGCAAGGAAGAGCTCAGGGCCATCCCGCGCGATGCGCGGCGAG 894

Qy 192 LeuGluGluTrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAsp 211

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Qy 212 LysGlyGlnAspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArg 231

Db 955 AATGACCCGGCCACTCGTCGGCCGGTGTCTCGCGCGCGCGCGCGC---CCCTACCCGCGC 1011

Qy 232 ArgGlyArgThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIlePro 251

Db 1012 CGCTGCCGACGGGCGCGCGCGCTGCGAGACAGACCCGTCGTCGGAGTCGCGC---CCG 1068

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Qy 312 GluGlyGlyIleLys---LeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIle 330

Db 1246 GAGGACGGGTACAAAGAACCGCGCTGCTGTCGTCGACGAGGAGCG-----GACAACCTC 1299

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Qy 351 ThrProGlnValIleGlnGluAsp---LysThrAlaTrpArgThrAsp---GluGluPhe 368

Db 1315 -----GAGGTGCTCCAGAAGCAGGTGAAGCTGCTGCTCAAGGGCGGAGAGGAGTTC 1368

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Qy 409 GlnIleGluAspLysLeuAspGly---LeuThrIleAspGluAlaIleLysThrAsnArg 427

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Qy 448 ThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeu 467

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Score:	1277.50	Matches:	234
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Query Match:	28.18%	Indels:	1
DB:	7	Gaps:	1
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Db	62	GGAGTCAACCCCTGTATCATTCGACGCTTCAGGAGTTTCCCCCGGTAGCAAGTTGGAT	121
QY	395	ProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeu	414
Db	122	CCTGAAGTATATGTTAATCAGACCAGTTCAATCAAAAGGGAGCACATAGAGAAAAACATG	181
QY	415	AspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHis	434
Db	182	GATGGACTAACTGTAGATGAAGCTATTGAGTGTAAATAGGCTGTTTATTATTAGACCATCAT	241
QY	435	AspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAla	454
Db	242	GATGCATTGTTCCTTACCTAAGCGGGATTAAATACA--ACAAAAACGAAGACTTATGCC	298
QY	455	SerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeu	474
Db	299	AGTCGGACTCTCCTTTTCTTCAAGATAATGGAACATTGAGGCCACTTGCAATTGAGTTG	358
QY	475	SerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAla	494
Db	359	AGCTTACCTCATCCACAAGGAGATAAACATGGTGCCACCAGCCTTGTTATTACACCAGCC	418
QY	495	AspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAsp	514
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QY	515	SerGlyValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPhe	534
Db	479	TCTGGCTATCATCAGCTTATCAGTCATTGGTTAAATACTCATGCAACAATAGAGCCATTT	538
QY	535	ValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisPro	554
Db	539	GTGATTGCTACAAATAGACATTTGAGCGCTACTTTCATCCAAATATTCAGACTTTTACAACCT	598
QY	555	HisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGly	574
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QY	575	GlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValVal	594
Db	659	GGAATACTTGAGCTGACAGTTTTTCCAGGGAAAATATGCCATGGAAATGTCATCTATTGTC	718
QY	595	TyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyVal	614
Db	719	TATAAAAACCTGGGTGTTCACTGAGCAAGGACTTCTGCTGATCTTCTTAAGAGAGGAGTA	778
QY	615	AlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyr	634
Db	779	GCAGTGTAGACTCAAGCCAGCCCTATGGCCTTAAACTTCTAATTGAGGATTATCCTTTT	838
QY	635	AlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsn	654
Db	839	GCTGTAGATGGGCTTGAGGTTTGGGCGCAATCGAAGCCTGGGTTGATGACTACTGTTCA	898
QY	655	TyrTyrTyrLysSerAsp	660
Db	899	TTCTATTACTCAACTGAT	916

CK255133	LOCUS	CK255133	935 bp	mRNA	linear	EST 30-JUL-2004
DEFINITION	EST738770 potato callus cDNA library, normalized and full-length	Solanum tuberosum cDNA clone POC186	5' end, mRNA sequence.			
ACCESSION	CK255133					
VERSION	CK255133.1	GI:39811714				
KEYWORDS	EST.					
SOURCE	Solanum tuberosum (potato)					
ORGANISM	Solanum tuberosum					
REFERENCE	1 (bases 1 to 935)					
AUTHORS	Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.					
TITLE	Generation of ESTs from potato callus tissue					
JOURNAL	Unpublished (2003)					
COMMENT	Other ESTs: EST738771					
	Contact: Robin Buell					
	The Institute for Genomic Research					
	9712 Medical Center Dr, Rockville, MD 20850, USA					
	Email: potato-array@tigr.org					
	Clones can be requested from the University of Arizona Genomics					
	Institute via http://genome.arizona.edu/orders/					
FEATURES	Seq primer: ATT TAG GTG ACA CTA TAG.					
source	Location/Qualifiers					
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	/lab_host="DH10B-Tona"					
	/clone_lib="potato callus cDNA library, normalized and					
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	/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;					
	supplier: RNA was isolated from Solanum tuberosum var.					
	Kennebec callus tissue grown on solid media."					
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Alignment Scores:						
Pred. No.:	2.75e-126	Length:	935			
Score:	1262.00	Matches:	229			
Percent Similarity:	86.41%	Conservative:	38			
Best Local Similarity:	74.11%	Mismatches:	38			
Query Match:	27.83%	Indels:	4			
DB:	7	Gaps:	2			
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QY	442	ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu	461			
Db	80	AAACGTATAAACACAACACTACC---ACACAGACGTATGCCTCAAGAACATGCTTTTCTTG	136			
QY	462	GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly	481			
Db	137	AATGAAGATGGATCATTTGAAGCCACTTGCTATTGAGTTAACT-----CGAGAAGAT	187			
QY	482	AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer	501			
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QY	502	IleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle	521			
Db	248	ATTTGGCAGCTTGCAAAAGCTTATGTACAGTGAATGATTTCTGGGTTTCCACGAGCTTGT	307			
QY	522	SerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGln	541			
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QY 627 LeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTTrpSerAlaIleLys 646  
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Db 779 TTAAGTATAGAGGACTATCCATACGCTGTTGATGGCTTAAAGA-TGGTCTGCAAC-AA 836  
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RESULT 14  
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LOCUS  
DEFINITION 45315.1 Common Scab-Challenged Tubers Solanum tuberosum cDNA clone  
45315 5', mRNA sequence.  
CV472045  
VERSION CV472045.1 GI:53696821  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 983)  
AUTHORS Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De  
Koeyer,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.  
TITLE Generation of ESTs from common scab-challenged potato tubers  
JOURNAL Unpublished (2004)  
COMMENT Contact: Barry Flinn  
The Canadian Potato Genome Project - BioAtlantech  
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
Email: bflinn@bioatlantech.nb.ca  
Seq primer: T3.  
Location/Qualifiers  
1. .983  
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/note="Vector: pBluescript II SK(+); Site\_1: EcoRI;  
Site\_2: XhoI; supplier: Pathogen-challenge series. Tubers  
from pathogen-free Solanum tuberosum var. Shepody, clone  
1756, were inoculated with Streptomyces scabei EF-35, by  
applying 1 ml of a spore stock (OD650 = 0.7). Tubers were  
placed in trays of sand and watered from the bottom for  
the remainder of the experiment. Inoculated tubers were  
sampled at 2 days, 1 week, 2 weeks and 4 weeks  
post-infection. Harvested tubers were washed in distilled  
water, blotted dry, cut into small pieces and frozen in  
liquid nitrogen. RNA was isolated from each sample  
collection, pooled and used for cDNA library  
construction."

ORIGIN  
Alignment Scores:  
Pred. No.: 2.32e-123 Length: 983  
Score: 1235.50 Matches: 237  
Percent Similarity: 86.11% Conservative: 42  
Best Local Similarity: 73.15% Mismatches: 41  
Query Match: 27.25% Indels: 6  
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GSLTS1172C01 of Silique of strain col-0 of Arabidopsis thaliana  
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LOCUS  
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
GSLTS1172C01 of Silique of strain col-0 of Arabidopsis thaliana  
(thale cress).  
ACCESSION BX181403



VERSION BX818403.1 GI:42470778
KEYWORDS HTC; GSLT CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 1473)
REFERENCE Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
AUTHORS Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1473)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_FF/Full
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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Score: 1233.00 Matches: 237
Percent Similarity: 66.60% Conservative: 92
Best Local Similarity: 47.98% Mismatches: 158
Query Match: 27.19% Indels: 7
DB: 3 Gaps: 6
US-10-731-642A-1 (1-862) x CNS0AAZ0 (1-1473)
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Dbb 61 GTCAGCAATCTTGACCCCAAGATCTACGGTCCACAACACTCCGCTCTTACTGACGACCAT 120
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Search completed: March 14, 2005, 10:27:33  
Job time : 6697 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:39:41 ; Search time 174 Seconds  
(without alignments)  
1916.020 Million cell updates/sec

Title: US-10-731-642A-1  
Perfect score: 4534  
Sequence: 1 MFLEKIVDAITGKDDGKKVK.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62.  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
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5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4534	100.0	862	ABP70404	Abp70404 Amino aci
2	3695	81.5	857	AAB46803	Aab46803 Potato LO
3	3610	79.6	859	ABO19443	Abol19443 Wine grap
4	3576	78.9	862	ABO19442	Abol19442 Wine grap
5	3022.5	66.7	880	AAO27492	Aao27492 Balsam pe
6	2911	64.2	878	AAB11500	Aab11500 C. sativu
7	2911	64.2	878	AAB86036	Aab86036 Cucumbe
8	2905	64.1	857	ABG30570	Abg30570 Glycine m
9	2779.5	61.3	864	ABW02705	Abw02705 Maize lip
10	2769.5	61.1	864	ADG93379	Adg93379 Maize lip
11	2769.5	61.1	864	ADG93381	Adg93381 Maize lip
12	2745.5	60.6	865	ABG30569	Abg30569 Glycine m
13	2734.5	60.3	887	ADG93389	Adg93389 Maize lip
14	2734.5	60.3	887	ADG93387	Adg93387 Maize lip
15	2724.5	60.1	887	AAO27494	Aao27494 Corn (Zea
16	2724.5	60.1	887	ADG93393	Adg93393 Maize lip
17	2724.5	60.1	887	ADG93391	Adg93391 Maize lip
18	2700.5	59.6	873	ADG93371	Adg93371 Maize lip
19	2700.5	59.6	873	ADG93373	Adg93373 Maize lip
20	2688	59.3	864	AAR24042	Aar24042 Lipoxigen
21	2686.5	59.3	853	AAR50220	Aar50220 Soybean l
22	2682	59.2	863	ADC53139	Adc53139 9'-specif
23	2680	59.1	862	AAU99691	Aau99691 Barley wi
24	2680	59.1	862	ABG30566	Abg30566 Wild type
25	2673	59.0	862	AAU99693	Aau99693 Barley wi

26	2673	59.0	862	5	AAU99692	Aau99692 Barley wi
27	2673	59.0	862	5	ABG30567	Abg30567 Mutant ty
28	2672.5	58.9	837	6	ADA48504	Ada48504 Rice prot
29	2656	58.6	839	5	ABG30568	Abg30568 Glycine m
30	2585.5	57.0	871	7	ADG93383	Adg93383 Maize lip
31	2585.5	57.0	871	7	ADG93385	Adg93385 Maize lip
32	2584.5	57.0	864	5	ABG30571	Abg30571 Barley lo
33	2563	56.5	865	2	AAR23797	Aar23797 Rice lipo
34	2563	56.5	865	2	AAR20670	Aar20670 Lipoxigen
35	2096.5	46.2	842	7	ADG93421	Adg93421 Maize lip
36	2096.5	46.2	842	7	ADG93419	Adg93419 Maize lip
37	1934	42.7	919	8	ADN72259	Adn72259 Thale cre
38	1906.5	42.0	491	7	AAE39891	Aae39891 Human lip
39	1906.5	42.0	491	8	ADQ48421	Adq48421 Lipoxigen
40	1843.5	40.7	892	7	ADG93395	Adg93395 Maize lip
41	1843.5	40.7	892	7	ADG93397	Adg93397 Maize lip
42	1840.5	40.6	807	7	ADG93413	Adg93413 Maize lip
43	1840.5	40.6	807	7	ADG93411	Adg93411 Maize lip
44	1814	40.0	896	8	ADN73207	Adn73207 Thale cre
45	1788	39.4	924	6	AAE38266	Aae38266 Rice dise

ALIGNMENTS

RESULT 1  
ABP70404  
ID ABP70404 standard; protein; 862 AA.  
XX  
AC ABP70404;  
XX  
DT 07-APR-2003 (first entry)  
XX  
DE Amino acid sequence of tobacco lipoxigenase-1 (LOX-1).  
XX  
KW Lipoxigenase-1; LOX-1; enzyme; plant; dioxygenation;  
KW polyunsaturated fatty acid; pentadiene; disease resistance; Solanacea;  
KW tobacco; tomato; potato; pepper.  
XX  
OS Nicotiana tabacum.  
XX  
PN WO200299112-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 06-JUN-2002; 2002WO-FR001943.  
XX  
PR 07-JUN-2001; 2001FR-00007470.  
PR 07-NOV-2001; 2001FR-00014358.  
(RHOB-) RHOBIO.  
PI Mene-Saffrane L, Esquerre-Tugaye M, Fournier J, Beffa R;  
PI Grosjean-Cournoyer M;  
XX  
DR WPI; 2003-156858/15.  
DR N-PSDB; ABZ68210.  
XX  
PT Reducing sensitivity of plants to diseases and pathogens, by  
PT overexpressing a lipoxigenase, also vectors and cassettes for the process  
PT and transformed plants.  
XX  
PS Claim 7; Page 39-41; 47pp; French.  
XX  
CC The present sequence represents a lipoxigenase-1 (LOX-1) gene. LOX-1 is  
CC an enzyme that catalyses the dioxygenation of polyunsaturated fatty acids  
CC having a pentadiene system. Overexpression of LOX-1 can be used to reduce  
CC the sensitivity of plants to diseases and attack by pathogens.  
CC Overexpression of LOX-1 improves resistance to viruses, bacteria, fungi  
CC and insects, in a wide range of crops, particularly the Solanaceae, e.g.  
XX tobacco, tomato, potato and pepper  
SQ Sequence 862 AA;

Query Match		100.0%;	Score 4534;	DB 6;	Length 862;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 862;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFLEKI	DAITGKDDGKKVKG	TVVLMKKNVLDFTDINASVLDGVLEFLGRRVSLELISSV	60
Db	1	MFLEKI	DAITGKDDGKKVKG	TVVLMKKNVLDFTDINASVLDGVLEFLGRRVSLELISSV	60
Qy	61	NADPANGLOGKRS	KAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAF	IIKNLHFS	120
Db	61	NADPANGLOGKRS	KAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAF	IIKNLHFS	120
Qy	121	EFFLKSLTLEDV	PHNGKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPD	TLRKYRENE	180
Db	121	EFFLKSLTLEDV	PHNGKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPD	TLRKYRENE	180
Qy	181	LVTLRGDGTGKLE	EDWRVYDYAYNDLGDPDKQDLSRPLGGSSEYPYPRRGRTGRKPT		240
Db	181	LVTLRGDGTGKLE	EDWRVYDYAYNDLGDPDKQDLSRPLGGSSEYPYPRRGRTGRKPT		240
Qy	241	KTDPNSESRIPL	MSLDIYVPRDERFGHIKLSDFLTFAKLSIVQLLPEFKALFDS	THNE	300
Db	241	KTDPNSESRIPL	MSLDIYVPRDERFGHIKLSDFLTFAKLSIVQLLPEFKALFDS	THNE	300
Qy	301	FDSFEDVLKLY	EGGIKLPGGPLLKAITDSIPLEILKELLSRDKGGLFKYPTPQVIOEDKT		360
Db	301	FDSFEDVLKLY	EGGIKLPGGPLLKAITDSIPLEILKELLSRDKGGLFKYPTPQVIOEDKT		360
Qy	361	AWRTDEEFGRE	MLAGVNPVIIISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTID		420
Db	361	AWRTDEEFGRE	MLAGVNPVIIISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTID		420
Qy	421	EAIKTNRLFIL	NHHIDILMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPD		480
Db	421	EAIKTNRLFIL	NHHIDILMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPD		480
Qy	481	GDQFGAVSKV	YTPADQGV	EGSIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNR	540
Db	481	GDQFGAVSKV	YTPADQGV	EGSIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNR	540
Qy	541	QLSALHPIYK	LLHPHFRET	MNINALARQILINGGGLLELTVPKYSMEMSAVYKDWVF	600
Db	541	QLSALHPIYK	LLHPHFRET	MNINALARQILINGGGLLELTVPKYSMEMSAVYKDWVF	600
Qy	601	PEQALPTDLI	KRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKSD		660
Db	601	PEQALPTDLI	KRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKSD		660
Qy	661	DAVQKDTELQ	AWWKELREEGHGDKKDEPWPKMQTVQELIDSCITITWIASALHAAVNFG		720
Db	661	DAVQKDTELQ	AWWKELREEGHGDKKDEPWPKMQTVQELIDSCITITWIASALHAAVNFG		720
Qy	721	QYPYAGYLP	PNRPTLSRNFMPEPGSP	EYEELKTNPDKVFLKTTITPQLQTLLGISLIEILSR	780
Db	721	QYPYAGYLP	PNRPTLSRNFMPEPGSP	EYEELKTNPDKVFLKTTITPQLQTLLGISLIEILSR	780
Qy	781	HSSDTLYLG	QRESPEWTKDQEP	LSAFARFGKKLSDIEDQIMQMNVDKWKNSRGPVKVPY	840
Db	781	HSSDTLYLG	QRESPEWTKDQEP	LSAFARFGKKLSDIEDQIMQMNVDKWKNSRGPVKVPY	840
Qy	841	TLLFPTSEGL	TGKIPNSVSI	862	
Db	841	TLLFPTSEGL	TGKIPNSVSI	862	

RESULT 2

AAB46803 standard; protein; 857 AA.

XX AC AAB46803;

XX DT 23-APR-2001 (first entry)

XX	Potato LOX protein.
DE	Potato; LOX protein; lipoxxygenase; arachidonic acid; mutant; plant;
XX	11-arachidonate-lipoxxygenase; 11-hydroperoxy-arachidonic acid.
KW	Solanum tuberosum.
XX	WO200104323-A2.
OS	18-JAN-2001.
XX	10-JUL-2000; 2000WO-EP006539.
PN	08-JUL-1999; 99DE-01031819.
XX	(IPBP-) IPB INST PFLANZENBIOCHEMIE.
XX	Feussner I, Hornung E, Rosahl S;
PI	WPI; 2001-081054/09.
XX	New nucleic acid encoding lipoxxygenase useful for producing 11-
DR	hydroperoxy- or hydroxy-arachidonic acid.
XX	Disclosure; Fig 3; 18pp; German.
PS	This invention describes a novel nucleic acid (I) encoding a potato
XX	lipoxxygenase protein, LOX, (II) is new. The invention also describes (1)
CC	(II), a sequence of 857 amino acids (aa), given in the specification; (2)
CC	a vector (III) comprising (I); (3) a host cell (IV) comprising (I) or
CC	(III); (4) a plant or part of a plant comprising (IV); (5) enhancing the
CC	specificity of a plant lipoxxygenase for position 11 of arachidonic acid
CC	comprises mutating at least one amino acid of the wild type lipoxxygenase;
CC	(6) producing 11-hydroperoxy-arachidonic acid or the reduced 11-hydroxy-
CC	derivative comprises treating arachidonic acid with (II) and further
CC	reducing the obtained hydroperoxy form to the hydroxy form; (7) the
CC	arachidonic acid derivative, comprising a hydroperoxy group or a hydroxy
CC	group at position 11. (II) is useful for producing 11- hydroperoxy-
CC	and/or 11-hydroxy-arachidonic acid. The lipoxxygenase is specific for
CC	position 11 of arachidonic acid
XX	Sequence 857 AA;
SQ	Query Match 81.5%; Score 3695; DB 4; Length 857;
	Best Local Similarity 80.0%; Pred. No. 6.4e-310;
	Matches 682; Conservative 84; Mismatches 85; Indels 2; Gaps 2;
Qy	10 ITGKDDGKKVKGTVVLMKKNVLDFTDINASVLDGVLEFLGRRVLSLELISSVNADPANGLO 69
Db	7 IGGHDSKKVKGTVVMMKKNALDFTDLAGSLTDKIFEALGQKVSFQLISSVQSDPANGLO 66
Qy	70 GKRSKAAYLENWLNTSTPIAAGESAFRVTFDWDDEEFGVPGAFIIKNLHFSEFFLKS LTL 129
Db	67 GKHSNPAYLENFLTTLTPLAAGETAFGVTFDW-NEEFGVPGAFIIKNTHINEFFLKS LTL 125
Qy	130 EDVPHGKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELVTLRGDGT 189
Db	126 EDVPHGKVHFCVNSWVYPSFRYKSDRIFFANQAYLPSETPELLRKYRENELVTLRGDGT 185
Qy	190 GKLEEDWRVYDYAYYNDLGDPDKQDLSRPVLGGSSEYYPYRRRGRTGRKPTKTDPNSESR 249
Db	186 GKREAWDRIYDYVNDLGNPDQGEQNVRTTLGGSADYPYRRRGRTGRPPTRTDPKSES 245
Qy	250 IPLLMSLDIYVPRDERFGHIKLSDFLTFAKLSIVQLLLPEFKALFDS THNEFDSFEDVLK 309
Db	246 IPLLMSLDIYVPRDERFGHLKMSDFLTVALKSIVQFILPELHALFDGTPNEFDSFEDVLR 305
Qy	310 LYEGGIKLPQGPLLKAITDSIPLLEILKELLSRSDGEGLFKYPTPQVIOEDKTAWRTDEEFG 369
Db	306 LYEGGIKLPQGPLFKALTAALPLEMMKELLRTDGE GILRFFTPLVIKDSKTAWRTDEEFA 365
Qy	370 REMLAGVNPVIIISRLQEFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEA IKTNRFL 429







Db 843 LYPTSEGLTGKIPNSVSI 862

RESULT 5

AAO27492 ID AAO27492 standard; protein; 880 AA.

AC AAO27492;

XX DT 06-NOV-2003 (first entry)

XX DE Balsam pear (Momordica charantia) lipoxigenase isozyme 2 protein.

XX KW Lipoxigenase; hydroperoxidation; polyunsaturated fatty acid; plant;  
KW fatty acid metabolite synthesis; signal molecule; growth regulation;  
KW development regulation; plant development; wound response;  
KW genetic mapping; hyperoxidation catalysis; Balsam pear; enzyme.

XX OS Momordica charantia.

XX PN US2003074693-A1.

XX PD 17-APR-2003.

XX PF 29-JAN-2002; 2002US-00059909.

XX PR 10-FEB-1999; 99US-0119597P.

XX PR 09-FEB-2000; 2000US-00501422.

XX PA (CAHO/) CAHOON E B.

XX PA (KINN/) KINNEY A J.

XX PA (KLEI/) KLEIN T M.

XX PA (LEEJ/) LEE J.

XX PA (PEAR/) PEARLSTEIN R W.

XX PA (RAFA/) RAFALSKI J A.

XX PA (SHEN/) SHEN J B.

XX PA (THOR/) THORPE C J.

XX PA (TING/) TINGEY S V.

XX PA (WENG/) WENG Z.

PI Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;

PI Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;

XX WPI; 2003-567325/53.

DR N-PSDB; AAL57712.

XX New isolated polynucleotides encoding plant lipoxigenases, useful in  
PT genetic mapping, particularly in catalyzing hyperoxidation of  
PT polyunsaturated fatty acids.

PS Claim 19; Page 23-25; 36pp; English.

XX This invention relates to novel nucleotide sequences which encode  
CC proteins which have lipoxigenase activity. Lipoxigenases are membrane  
CC bound ubiquitous enzymes which catalyse the hydroperoxidation of  
CC polyunsaturated fatty acids in the first step of fatty acid metabolite  
CC synthesis. Products of this pathway are found as signal molecules  
CC involved in growth and development regulation. A knowledge of the amino  
CC acid sequence of lipoxigenases may allow the understanding of plant  
CC development and wound response. The polynucleotides, polypeptides and  
CC lipoxigenases of the invention may therefore be useful in genetic mapping  
CC and particularly for catalysing hydroperoxidation of polyunsaturated  
CC fatty acids. The present sequence is the amino acid sequence of the  
CC Balsam pear (Momordica charantia) lipoxigenase protein 2 of the invention  
XX

SQ Sequence 880 AA;

Query Match 66.7%; Score 3022.5; DB 6; Length 880;  
Best Local Similarity 65.4%; Pred. NO. 1.1e-251;  
Matches 554; Conservative 132; Mismatches 156; Indels 5; Gaps 4;

QY 16 GKVKGTIVLMKKNVLDFTDINASVLDGVLEFLGRRVSLELISSVNADPANGLOQKRSKA 75

Db 39 GKIKIGTVVLMRSNVLDFTTEFHSSLLDGVTELLGGGISQLISATHA--SNDSRGKVGKG 96  
QY 76 AYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHSEFFLKSLTLEDVPH 135  
Db 97 AFLERWLTSVPPLFAGESVFQVNFWD-EENFGFPGAFFIKNGHTSEFFLKSVTLEDVPGF 155  
QY 136 GKVHFVCSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYRENELVTLRGDGTGKLEEW 195  
Db 156 GRVHFDCSWVYPSRRYKKDRIFFANHTCLPIDTPDSLRKYREEELNLRGDGTGERKEW 215  
QY 196 DRVYDAYYNDLGDPPDKQDLSRPVLGGSSEYYPYPRRGTGRKPTKTDPNSESRIPLMS 255  
Db 216 DRIYDYVYNDLCDPNGGPNLVRPIILGSDQYYPYPRRGTGRPPARKDHKYESRLSDVMS 275  
QY 256 LDYVPRDERFGHIKLSDFLTALKSIVQLLLPEFKALFDSHNEFDSFEDVCLKYEGGI 315  
Db 276 LNIYVPRDENFGHLKMADFLGNLTCLKVLSTSIQPGLESIFDSTPGGEFDKFKEVDLFERGF 335  
QY 316 KLPQGPILLKAITDSIPLLEILKELRSDEGLFKYPTQVIQEDKTAWRTDEEFGREMLAG 375  
Db 336 PIPLN-IPKNLTEDLAPPLFKAFLESDGERFLKYPTPOVIKDKLGWRTDEEFAREMIAG 394  
QY 376 VNPVIISRLQEFFPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKTNRLFILNHH 435  
Db 395 VNPLIIRRELVFPPLSKLDPHVYGNQNSTMTETEEQIKHGLDGLTVDEAIKENKLYILDH 454  
QY 436 ILMPYLRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPDGQFGAVSKVYTPAD 495  
Db 455 ALMPYLRIN-STSTKTYATRTLLFLKDDSTLKLAIELSLPHPDGDEHGAISKLYFP 513  
QY 496 QGVEGSIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQLSALHPIYKLLHPH 555  
Db 514 GRVESAIWQLAKAYAVVNDSGVHQLNSHWLHTHAVLEPFVITTHRRLSVLHPIHKLLAPH 573  
QY 556 FRETMINALARQILINGGGLLELTVPFPAKYSMEMSAVVYKDWVPEQALPTDLIKRGVA 615  
Db 574 YKDTMFINASARQVLINAGGLIESTQFPKAYAMELSSYIYKEWKFDEALPTNLIKRGVA 633  
QY 616 VEDSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSDDAVQKDTLOAWWKE 675  
Db 634 IEDSGSPHGVRLLLINDYPFAVDGLEIWSAIKTWTDYCSLYYKDDDAIRNDVELOSWWKE 693  
QY 676 LREEGHGDKKDEPWPKMQTVQELIDSCITITIWIASALHAAVNFGQYPYAGYLPNRP 735  
Db 694 LREKGTDKKDEPWPKMQTFSELIESCTIIIISSALHAAVNFGQYPYGGYVPNRP 753  
QY 736 RNFMPEPGSPYEELKTNPKVFLKTTTPQLQTLGLISLIEILSRHSSDTLYLGQRESPE 795  
Db 754 RRFMEVGTAEYKEVESNPEKAFRLRTISSQIVALLGLSIIELSKHASDEVYLGQASIE 813  
QY 796 WTKDQEPLSAFARFGKLSIDIEDQIMQMNVDKWKNSRSGPVKVPYTLTFPTSEGLTGKG 855  
Db 814 WTSKSAIEAFEKFGKELFEVEDRIMRNQDVNLKNRAGPVNMPYTLVPSSTEGLTGRG 873  
QY 856 IPNSVSI 862  
Db 874 IPNSISI 880

RESULT 6  
AAB11500  
ID AAB11500 standard; protein; 878 AA.  
XX  
AC AAB11500;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE C. sativus LOX protein.  
XX  
KW LOX; lipoxigenase; cucumber; plant; 6-hydroperoxy-gamma-linolenic acid;  
KW 9-hydroperoxy-gamma-linolenic acid; 6,9-hydroperoxy-gamma-linolenic acid;  
KW gamma-linolenic acid.





Query Match		64.2%;	Score 2911;	DB 4;	Length 878;
Best Local Similarity		62.3%;	Pred. No. 4.8e-242;		
Matches 534;		Conservative 140;	Mismatches 175;	Indels 8;	Gaps 6;
Qy	6	IVDAITGKDGKKVKGTVVLMKQNVLDFTDINASVLDGVLEFLGRRVSLELISSVNADPA	65		
Db	30	ILDRVSSL-GGNKIKGVILMRSNVLDFTTFHNSLLDNFTELLGGVSFQLISATHT--S	86		
Qy	66	NGLQKRSKAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHFSEFFLK	125		
Db	87	NDSRGKVGNAKAYLERWLTSIPPLFAGESVFQINFQW-DENFGFPGAFFIKNGHTSEFFLK	145		
Qy	126	SLTLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELVTLR	185		
Db	146	SLTLDDVPGYGRVHFDCNSWVYPSGRYKDKDRIFFFANHVYLPSTQPNPLRKYREELWNL	205		
Qy	186	GDGTGKLEEDRVYDYAYYNDLGDPDKGQDLSRPVLGGSSEYYPYRRGRTGRKPTKTDPN	245		
Db	206	GDGTGERKEWDRIYDYVDYNDIADPDVGD--HRPILGGTTEYPYPRGRTGRPSRRDHN	263		
Qy	246	SESRIPLMSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLLPEFKALFDSHTNEFDSFE	305		
Db	264	YESRLSPIMSLDIYVPKDENFGHLKMSDFLGYTLKALSISIKPGLQSFVDVTPNEFDNF	323		
Qy	306	DVLKLYEGGIKLPGQPLLKAITDSIPLEILKELLRSDGEGLFKYPTPOVIEDKTAWRTD	365		
Db	324	EVDNLFERGPPIPN-AFKTLTEDLTPLPKALVRNDGEKFLKFTPEVVKDNKIGWSTD	382		
Qy	366	EEFGREMLAGVNPVIISRLQEFPPKSLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKT	425		
Db	383	EEFAREMLAGNPLLIRLEAFPTSKLDPNVYGNQNSTITEEHKHLGLDGLTVDEAMQ	442		
Qy	426	NRLFILNHHDIILPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAJELSLPHPDGQFG	485		
Db	443	NRLYIVDFHDALPYLTRMN-ATSTKTYATRTLKDDGTGLKPLVIELALPHPGDQLG	501		
Qy	486	AVSKVYTPADQGVGEGSIWLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIAIATNRQLS	545		
Db	502	AISKLYFAENGVSQKSIWLAKAYVTVNDVGYHQLISHWLTHAVLEPFVIAIATHRQLSV	561		
Qy	546	HPIYKLLHPHFRETMINALARQIILINGGELLELTVPKAKYSMEMSAVVYKDWVPEQAL	605		
Db	562	HPIHKLVLPHYKDTMFINASARQVLINANGLIETHTHYPKYSMELSSILYKDWTFPDQAL	621		
Qy	606	PTDLIKRGVAVEDSSSPLGIRLLIQDYPPYAVDGLKIWSAISKSWVTEYCNYYKSDDAVQK	665		
Db	622	PNNLMKRGLAVEDSSAPHGLRLLINDYPPAVDGLDIWSAIAKTWQDYCCLYKDDNAVQN	681		
Qy	666	DTELQAWKELREEGHGDKDEPWPMPKMTVQELIDSCITIIWIASALHAAVNFQYPPYA	725		
Db	682	DFELQSWNELREKGHADKKHEPWPMPKMTLSIELIESCTTIIWIASALHAAVNFQYPPY	741		
Qy	726	GYLPNRPILSRNFMPEPGSPYEYELKTNPDKVFLKTIITPQLOTLLGLISLIEILSRHSSDT	785		
Db	742	GYILNRPITTSRRFMPEVGTAEYKELESNEPEKAFRLTICSELQALVSIIEILSKHASDE	801		
Qy	786	LYLQRESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPVKVPYTLTLP	845		
Db	802	VYLGQRASIDWTSKIALEAFEKFGKNLFEVENRIMERNEVNLKNRSGPVNLPYTLTLP	861		
Qy	846	TSEGGLTGKIPNSVSI	862		
Db	862	SSNEGLTGRGIPNSISI	878		

RESULT 8  
ABG30570  
ID ABG30570 standard; protein; 857 AA.  
XX  
AC ABG30570;  
XX  
DT 07-OCT-2002 (first entry)

XX	Glycine max low-lipoxygenase 3 (LOX-3).	
DE		
XX		
KW	Lipoxygenase-1; LOX-1; beverage; malt; beer; organoleptic property;	
KW	brewing; trans-2-nonenal; flavour stability; storage; shelf-life;	
KW	low-lipoxygenase 3.	
XX		
OS	Glycine max.	
XX		
PN	WO200253721-A1.	
XX		
PD	11-JUL-2002.	
XX		
PF	22-JAN-2001; 2001WO-IB000207.	
XX		
PR	29-DEC-2000; 2000US-00751687.	
PR	29-DEC-2000; 2000WO-IB002045.	
XX		
PA	(CARL-) CARLSBERG RES LAB.	
PA	(HETB ) HEINEKEN TECH SERVICES BV.	
PA	(BRAS-) BRASSERIES KRONENBOURG SA.	
XX		
PI	Douma AC, Doderer A, Cameron-Mills V, Skadhauge B, Bech LM;	
PI	Schmitt N, Heistek JC, Van Mechelen JR;	
XX		
DR	WPI; 2002-557742/59.	
XX		
PT	Novel barley plants having low lipoxygenase activity useful in the	
PT	production of plant products such as malt or brewed beverages,	
PT	particularly beer having increased stability and flavor.	
XX		
PS	Disclosure; Fig 22A-B; 112pp; English.	
XX		
CC	The invention describes a barley plant (I) having a mutant lipoxygenase-1	
CC	(LOX-1) protein, the plant or plant portion characterised by a reduction	
CC	or absence of LOX activity as compared to a non-mutated control, or	
CC	comprising a heterologous nucleic acid sequence expressing an antisense	
CC	sequence to a transcribed region of barley lox-1 gene, operably linked to	
CC	a promoter and a transcription terminator sequence. (I), a plant (II)	
CC	produced using (I) or a plant product (III) is useful in the manufacture	
CC	of a beverage, preferably malt or beer, for stabilising organoleptic	
CC	properties of a brewed product over a measured period of time as compared	
CC	to a control brewed product produced using a non-mutated barley plant or	
CC	its portion, grain or plant progeny, or plant product, and for the	
CC	manufacture of a brewed product having reduced levels of free trans-2-	
CC	nonenal over a measured period of time or under conditions of elevated	
CC	storage temperature, as compared to a control brewed product produced	
CC	using a non-mutated barley plant or its portion, grain or plant product.	
CC	Beer with significantly enhanced flavour stability, both during storage	
CC	and on exposure to elevated storage temperatures is obtained. These	
CC	properties enhance the quality of beer and are useful to extend its shelf	
CC	-life and reduce the need to cool beer during transport and storage. This	
CC	is the amino acid sequence of the Glycine max low-lipoxygenase 3 (lox-3)	
CC	protein	
XX		
SQ	Sequence 857 AA;	

Query Match 64.1%; Score 2905; DB 5; Length 857;  
Best Local Similarity 63.3%; Pred. No. 1.5e-241;  
Matches 548; Conservative 122; Mismatches 160; Indels 36; Gaps 9;

Qy	16	GKKVKGTVVLMKKNVLDFT-----DINASVLDGVLEFLGRRVSLELISSVNA	62
Db	9	GHKIKGTVVLMRKNVLDVNSVTSVGGIIGQGLDLVGSTLDTLTAFLGRSVSLQISATKA	68
Qy	63	DPANGLQKRSKAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHFSEF	122
Db	69	D-ANG-KGKLGKATFLEGIITSPLTGAGQSAFKINFEDDGS-GIPGAFYIKNFMQTEF	125
Qy	123	FLKSLTLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELV	182
Db	126	FLVSLTLEDIPNHGSIHFVCNSWIYNAKLFKSDRIFFANQTYLPSETPAPLVKYREEELH	185

QY 183 TLRGDCGKLEWDRVYDYAYVNDLGDGDKQDLSPVLGSGSEYYPRRGRTRGKPKTK 242  
Db 186 NLRGDCGKERKEWERYIDYDVNDLGDGDKGENHARPVLGNDTFPPYRRGRTRGKPKTK 245  
QY 243 DPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTALKSIVQLLLPEFKALFD--STHNE 300  
Db 246 DPNSESR-----SNDVYLPRDEAFGLKSSDFLTGLKSVSQNVLPLLQSAFDLNFTRP 300  
QY 301 FDSFEDVLKYEGGIKLPQGPLLKAITDSI-----PLEILKELLRSDGGLFKYPTPQVIO 356  
Db 301 FDSFDEVHGLYSGGIKLP-----TDIISKISPLPVLKEIFRTDGEQALKFPPPKVIO 352  
QY 357 EDKTAWRDDEFGREMLAGVNPVIRLQEFPPPKSLDPKIYGNQNSTITREQIEDKLDG 416  
Db 353 VKSAMWTDEEFAREMLAGVNPILIRCLKDFPPRSKLDQVYGDHTSQITKEHLEPNLEG 412  
QY 417 LTIDEAIKTNRLFILNHHDIIMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSL 476  
Db 413 LTVDEAIQNKRLLFLDDHDPIMPYLRRIN-ATSTKAYATRTILFLKNDGTLRPLAIELSL 471  
QY 477 PHPDGDQFGAVSKVYTPADQGVESIQWLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVI 536  
Db 472 PHPQGDQSGAFSQVFLPADEGVESSIWLAKAYVVVNDSCYHQLVSHWLNTHAVVEFII 531  
QY 537 ATNRQLSALHPIYKLLHPHFRETNNALARQILINGGGELLETLVFPKAYSMEMSAVVYK 596  
Db 532 ATNRHLSVVHPIYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTLWGGRYSVEMSAVVYK 591  
QY 597 DWVPPEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYY 656  
Db 592 DWVFTDQALPADLIKRGMAIEDPSCPGRIRLVIEDPYTYVDGLEIWDAIKTVWHEYVFLY 651  
QY 657 YKSDDAVQKDTLQAWWKELREEGHGDKDEPWWPKMQTVQELIDSCITITIWIASALHAA 716  
Db 652 YKSDDTLREDPELQACWKELVEVGHGDKKNEPWWPKMQTREELVEACAIITWASALHAA 711  
QY 717 VNFQYQYAGYLPNRPRTLNRNFMPEGSPYEELKTNPDKVFLLKTIIPQLQTLIGISLIE 776  
Db 712 VNFQYQYPYGLILNRPRTLNRNFMPEKGAIEYELRNKPKQAYLKTITPKFQTLIDLSVIE 771  
QY 777 ILSRHSSDTLYLQORESPETWKDQEPLSAFARFGKLSDIEDQIMQMNVDKWKNRSGPV 836  
Db 772 ILSRHASDEVYLGERNPNWTSDTTRALEAFKRFGNKLAQIENKLSERNNDEKLRNCGPV 831  
QY 837 KVPYTLFFPTSEGGLTGKIPNSVSI 862  
Db 832 QMPYTLLLPSSKEGLTFRGIPNSISI 857

RESULT 9  
ABW02705

ID ABW02705 standard; protein; 864 AA.

AC ABW02705;

DT 11-MAR-2004 (first entry)

DE Maize lipoxxygenase (CSSAP92) protein.

KW Maize; lipoxxygenase; CSSAP92; aflatoxin; gene therapy; plant protectant;  
KW enzyme.

OS Zea mays.

PN US6627797-B1.

XX 30-SEP-2003.

XX 16-MAR-2001; 2001US-00810268.

PR 21-MAR-2000; 2000US-0190950P.

PA (TEXA ) UNIV TEXAS A & M SYSTEM.

PA (PION-) PIONEER HI-BRED INT INC.  
XX Duwick J, Maddox JR, Keller NP;  
PI WPI; 2003-874315/81.  
XX N-PSDB; AAD64728.  
DR  
XX New maize lipoxxygenase polynucleotide, designated CSSAP92, useful for  
PT altering lipoxxygenase concentration in plants, for decreasing  
PT accumulation of aflatoxin in plants, or for increasing the resistance of  
PT plants to pathogens.  
XX  
PS Claim 1; SEQ ID NO 3; Opp; English.  
XX  
CC The invention relates to maize lipoxxygenase polynucleotide, designated  
CC CSSAP92. The nucleic acid molecule and methods are useful in altering  
CC lipoxxygenase concentration in plants, in decreasing accumulation of  
CC aflatoxin in plants, or in increasing the resistance of plants to  
CC pathogens. The invention is useful in gene therapy. The present sequence  
CC is the maize lipoxxygenase protein  
XX  
SQ Sequence 864 AA;  
Query Match 61.3%; Score 2779.5; DB 7; Length 864;  
Best Local Similarity 60.6%; Pred. No. 1.1e-230;  
Matches 525; Conservative 124; Mismatches 207; Indels 11; Gaps 5;  
QY 3 LEKIVDAITGKDDGKKVGTIVLMKKNVLDFTDINASVLGVLGFLGRRVSLELISSVNA 62  
Db 2 LSGIIDGLTGANKHARKGTIVLMRKNVLDLNDFGATVVDISSEFLGKGTQCQLISSTLV 61  
QY 63 DPANGLQGRSKAAAYLENWLTNSTPIAAGESAFRVTFDWDDEFGVPGAFIINKLHFSEF 122  
Db 62 DANNGNRGRVGAEANLEQWLTSLTSGESKFGVTFDWEVEKLGVPGAVVKNHAAEF 121  
QY 123 FLKSLTLEDVNPNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYRENELV 182  
Db 122 FLKTIITLDDVPGRGAVTFVANSWVYPAGKYRYNRVFFSNDTYLPSQMPAALKPYRDDLR 181  
QY 183 TLRGDG-TGKLEWDRVYDYAYVNDLGDGDKQDLSPVLGSGSEYYPRRGRTRGKPKTK 241  
Db 182 NLRGDDQQGPYQEHDRVRYDVNDLGEPDGNN--PRPILGGSADHPYPRRCRTGRKPKTK 239  
QY 242 TDPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTALKSIVQLLLPEFKALFDSTHNEF 301  
Db 240 TDPNSDSRLSLVE--QIYVPRDERFGHLKMSDFLGYSIKAITQGIIPAVRTYVDTTPGEF 297  
QY 302 DSFEDVLKYEGGIKLPQGPLLKAITDSIPLEILKELLRSDGGLFKYPTPQVIOEDKTA 361  
Db 298 DSFQDIINLYEGGIKLPKIQALEDMRKLFPQLVKDLLPAGGDYLLKLPIPIQIIQEDKNA 357  
QY 362 WRTDEEFGREMLAGVNPVIRLQEFPPPKSLDPKIYGNQNSTITREQIEDKLDGLTIDE 421  
Db 358 WRTDEEFAREVLAGVNPVITLTFEFPKSTLDPSKYGDHTSTITAETHIEKNLEGLTVQQ 417  
QY 422 AIKTNRLFILNHHDIIMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPDG 481  
Db 418 ALDGNRLYILDHHRFMPFLIDVNNLEGNFIYATRTLFFLRGDRGLAPLAIELSEPYIDG 477  
QY 482 DQFGAVSKVYTPADQGVESIQWLAKAYAAVNDSGVHQLISHWLNTHAAIEPFIATNRQ 541  
Db 478 DLTVAKSKVYTPASSGVEAWVQLAKAYAVAVNDSGVHQLVSHWLNTHAVMEPFIATNRQ 537  
QY 542 LSAHPYIKLLHPHFRETNNALARQILINGGGELLETLVFPKAYSMEMSAVVYKDWVFP 601  
Db 538 LSVTHPVHKLSSHFRDWTMTINALARQTLINGGGIFEMTVFPGYALGMSSVVYKSWNFT 597  
QY 602 EQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKSD 661  
Db 598 EQGLPADLVKRGVAVADPSSPYKVRLLIEDYPYASDGLAIWHAIEQWVGEYLAIYPPDG 657  
QY 662 AVQKDTLQAWWKELREEGHGDKDEPWWPKMQTVQELIDSCITITIWIASALHAAVNFQ 721

Db	658	ALRGDEELQAWKEVREVGHGDHDKDAPWWPKMQAVSELASACTTIIWIASALHAAVNFGQ	717
Qy	722	YPYAGYLPNRPTLSRNFMPGSPGYEELKTNPKVFLKTTTPQLQTLGSLIEILSRH	781
Db	718	YPYAGYLPNRPTVSRMRMPGSPGYEELERDPERGFIHTITSQIQTIIGSLIEILSKH	777
Qy	782	SSDTLYLGQRESPEWTKDQEPLSAFARFGKKLSLSDIEDQIMQMNVDKWKNSRGPVKVPYT	841
Db	778	SSDEVYLGQDTPWTS DARALAAFRFS DALVKIEGKVVGENDPQLNRNGPAEFPYM	837
Qy	842	LLFP-TSE-----GGLTGKGINPSVSI	862
Db	838	LLYPNTSDHSGAAAGLTAKGINPSISI	864
RESULT 10			
ADG93379			
ID	ADG93379	standard; protein; 864 AA.	
XX			
AC	ADG93379;		
XX			
DT	11-MAR-2004	(first entry)	
XX			
DE	Maize lipoxxygenase (LOX) polypeptide #5.		
XX			
KW	Maize; lipoxxygenase; LOX; corn; plant; plant pathogen defence system;		
KW	plant development; tissue healing; mycotoxin; aflatoxin;		
KW	sterigmatocystin.		
XX			
OS	Zea mays.		
XX			
PN	US2003166855-A1.		
XX			
PD	04-SEP-2003.		
XX			
PF	25-APR-2002; 2002US-00132350.		
XX			
PR	27-APR-2001; 2001US-0286889P.		
PR	13-JUL-2001; 2001US-0305366P.		
XX			
PA	(PION-) PIONEER HI-BRED INT INC.		
XX			
PI	Navarro Acevedo PA, Duwick JP, Kolomiets MV, Simmons CR;		
XX			
DR	WPI; 2003-898106/82.		
DR	N-PSDB; ADG93378.		
XX			
PT	New lipoxxygenase polypeptides and polynucleotides, useful for enhancing		
PT	resistance to pathogens, e.g. fungi, viruses, nematodes or insects, for		
PT	promoting healing of damage tissues, or for modulating plant growth and		
PT	development.		
XX			
PS	Disclosure; SEQ ID NO 10; 151pp; English.		
XX			
CC	The invention relates to maize lipoxxygenase (LOX) polypeptides and		
CC	polynucleotides encoding the polypeptides. The LOX polypeptides and		
CC	polynucleotides are useful in modulating plant pathogen defence systems		
CC	(particularly enhancing resistance to fungi, viruses, nematodes and		
CC	insects) and plant development, and for promoting healing of damaged		
CC	tissues. LOX proteins may also be used to inhibit the production of		
CC	mycotoxins of fungi (e.g. aflatoxin) and sterigmatocystin producing		
CC	fungus in plants susceptible to contamination by the mycotoxins. This		
CC	sequence represents a maize LOX polypeptide of the invention.		
XX			
SQ	Sequence 864 AA;		
Query Match			
Best Local Similarity 61.1%; Score 2769.5; DB 7; Length 864;			
Matches 524; Conservative 124; Mismatches 208; Indels 11; Gaps 5;			
Qy	3	LEKIVDAITGKDDGKKVGTVMKKNVLDFTDINASVLDGVLEFLGRRVSLIEISSVNA	62
Db	2	LSGIIDGLTGANKHARLKGTVLMRKNVLDLNDFGATVWDSISEFLGKGVTCQLISSTLV	61

Qy	63	DPANGLOGKRKAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHSEF	122
Db	62	DANNGNRGRVGALEANLEQWLTSLPSLTGSGKFGVTFDWEVEKLGVPGAVVKNHAAEF	121
Qy	123	FLKSLTLEDVPHNGKVFVNCNSVVPANKYKSDRIFFANQAYLPSETPDTLRKYRENELV	182
Db	122	FLKTTILDDVPGRGAVTFVANSVVPAGKYRYNRVFFSNDTYLPQMPAALKPYRDELRL	181
Qy	183	TLRGDG-TGKLEEDWRVDYAYVNDLGDGDKQDLSRVLGSGSEYPYPRRGRTGRKPTK	241
Db	182	NLRGDDQQGPYQEHDRVRYDVYNDLGEPDGGN--PRPILGGSADHPYPRRCRTGRKPTK	239
Qy	242	TDPNSESRIPLMLSDIYVPRDERFGHIKLSDFLTALKSIVQLLPEFKALFDSTHNEF	301
Db	240	TDPNSDSRLSLVE--QIYVPRDERFGHLKMSDFLGYSIKAITQGIIPAVRTYVDTTPGEF	297
Qy	302	DSFEDVLKLYEGGIKLPGQPLLKAITDSIPLEILKELLRSDEGLFKYPTPQVIQEDKTA	361
Db	298	DSFQDIINLYEGGIKLPKIQALEDMRKLFPLOLVKDLLPAGGDYLLKLPQPQIIQEDKNA	357
Qy	362	WRTDEEFGREMLAGVNPVVIISRLQEPFPPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDE	421
Db	358	WRTDEEFAREVLAGVNPVMVITRLTEFPFPPKSTLDPSPKYGDHTSITTAHIEKNLEGLTVQQ	417
Qy	422	AIKTNRLFILNHHDIILMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPDG	481
Db	418	ALDGNRLYILDHHRFMPFLIDVNNLEGNFIYATRTLFFLRGDRGLAPLAIELSEPYIDG	477
Qy	482	DQFGAVSKVYTPADQGVESIWOLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQ	541
Db	478	DLTVAKSKVYTPASSGVEAWWQALAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVIATNRQ	537
Qy	542	LSALHPIYKLLHPHFRETNNINALARQILINGGELLELTVPFPAKYSMEMSAVVYKDWVFP	601
Db	538	LSVTHPVHKLSSHFRDTMTINALARQTLINGGGIFEMTVFPGKYALGMSVVYKSWNFT	597
Qy	602	EQALPTDLIKRGVAVEDSSSPGLIRLLIQDYPYAVDGLKIWSAISKSWTEYCNYYKSD	661
Db	598	EQGLPADLVKRGVAVADPSSLYKVRLLIEDYPYASDGLAIWHAIEQWVGEYLAIYPPDDG	657
Qy	662	AVQKTELOAWWKELREEGHGDKDEPWPQMTVQELIDSCITTIWIASALHAAVNFGQ	721
Db	658	ALRGDEELQAWWKEVREVGHGDHKOAPWWPKMQAVSELASACTTIWIASALHAAVNFGQ	717
Qy	722	YPYAGYLPNRPTLSRNFMPGSPGYEELKTNPDKVFLKTTIPQLQTLGSLIEILSRH	781
Db	718	YPYAGYLPNRPTVSRRRMPEPGSKEYEELERDPERGFIHTITSQIQTIIGISLIEILSKH	777
Qy	782	SSDTLYLGQRESPEWTKDQEPLSAFARFGKLSLSDIEDQIMQMNVDKWKNRSGPVKVPYT	841
Db	778	SSDEVYLGQDTPWTS DARALAAFRFS DALVKIEGKVVGENDPQLNRNGPAEFPYM	837
Qy	842	LLFP-TSE-----GGLTGKGINPSVSI	862
Db	838	LLYPNTSDHSGAAAGLTAKGINPSISI	864
RESULT 11			
ADG93381			
ID	ADG93381	standard; protein; 864 AA.	
XX			
AC	ADG93381;		
XX			
DT	11-MAR-2004	(first entry)	
XX			
DE	Maize lipoxxygenase (LOX) polypeptide #6.		
XX			
KW	Maize; lipoxxygenase; LOX; corn; plant; plant pathogen defence system;		
KW	plant development; tissue healing; mycotoxin; aflatoxin;		
XX			
OS	Zea mays.		







QY	115	KNLHSEFFFLKSLTLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLR	174
Db	120	RNLQHAEFFFLKSLTLEGVPGRGTVVFVANSWIYPHNLYSQERVFVFANDTYLPSKMPAALV	179
QY	175	KYRENELVTLRG-DGTGKLEEWDRVYDYAYYNDLGDPPDKQDLSRPPVLGGSSEYPYPRRG	233
Db	180	PYRQDELKILRGDDNPGPYKEHDRVYDYNDLGEPPDKGEDHARPVLGGSQEHYPYPRRC	239
QY	234	RTGRKPTKTDPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFAKLSIVQLLPEFKAL	293
Db	240	RTGRRPTETDPNSESRL-FLNLNIIYVPRDERFGHLKMSDFLGYSLKAIIEAVLPTLGRF	298
QY	294	FDSTHNEFDSFEDVLKLYEGGIKLPQGILLKAITDSIPLEILKELLRSDG--EGLFKYPT	351
Db	299	VDDTPKEFDSFEDILGLYEPGPEAPNPNPLVAEVRKRIPISEFLRSIL-PDGSHDHPLKMPL	357
QY	352	PQVIQED-----KTAWRTDEEFGREMLAGVNPVVISRLQEPFPKSKLDPKIYGNQNS	403
Db	358	PNIIRSDVLKKAPEFKFGWRTDEEFARETLAGVNPVLIKRLTEFFPAKSTLDPSQYGDHTS	417
QY	404	TITREQIEDKLDGLTIDEAIKTNRLFILNHHDIILMPYLRRINTSTDTKTYASRTLLFLQD	463
Db	418	KITEAHIQHNMEGLSVQNALKKNRFLILDHHDHFMPLYLNKINELEGNFIYASRTLLFLKD	477
QY	464	NGTLKPSAIELSLPHPDGQFGAVSKVYTPADQGVGSIWQLAKAYAAVNDSGVHQLISH	523
Db	478	DGTLKPLAVELSLPHPDGQGHGAVSKVYTPAHSGAEGHVWQLAKAYACVNDSAWHQLISH	537
QY	524	WLNTHAAIEPFFVIATNRQLSALHPYIKLLHPHFRETMINALARQILINGGGLLELTVFP	583
Db	538	WLNTHAVIEPFFVIATNRQLSVVHPVKLLSPHYRDTLNINALAQTLINADGIFERTVFP	597
QY	584	AKYSMEMSAVVYKDWVFEQALPTDLIKRGVAVEDSSSPGLIRLLIQDYPYAVDGLKIWS	643
Db	598	AKYALGMSDDVYKSWNFNEQALPADLVKRGVAVPDQSSPYGVRLLIKDYPAVDGLVIWW	657
QY	644	AIKSWVTEYCNYYKSDDAVQKDTLQAWWKELREEGHGDKDEBPWPKMQTVQELIDSC	703
Db	658	AIERWVKEYLDVYYPNDGELQRDVELQAWWKEVREEAHGDLKDRDWPRMDAVQRLARAC	717
QY	704	TITIWIASALHAAVNFQYYPYAGYLPNRPVSRPMPEPGSDDYKYLEAGQKEADAVFIR	777
Db	718	TTVIWVASALHAAVNFQYYPYAGYLPNRPVSRPMPEPGSDDYKYLEAGQKEADAVFIR	777
QY	761	TITPOLQTLGISLIEILSRHSSDTLYLGQRESPE-WTKQDEPLSAFARFGKLSDIEDQ	819
Db	778	TITSQFQTLGISLIEILSKHSSDEVYLGQDEPERWTSARALDAFRFRFGSRLVEIEKR	837
QY	820	IMQMVNDEKWNRSQVYKPYTLLFPTSEG-----GLTGKGIPIINSVSI	862
Db	838	IRTWNDSPTLKNRKGVPVEMPYMLLYPNTSDVTGEKGEGLTAMGIPNSISI	887
RESULT 14			
ID	ADG93387		
XX	ADG93387	standard; protein; 887 AA.	
AC	ADG93387;		
DT	11-MAR-2004	(first entry)	
XX	Maize	lipoxigenase (LOX) polypeptide #9.	
XX	Maize;	lipoxigenase; LOX; corn; plant; plant pathogen defence system;	
KW	plant development;	tissue healing; mycotoxin; aflatoxin;	
KW	sterigmatocystin.		
OS	Zea mays.		
XX	US2003166855-A1.		
PN	04-SEP-2003.		
XX			
PD			

XX	25-APR-2002;	2002US-00132350.	
PF	27-APR-2001;	2001US-0286889P.	
XX	13-JUL-2001;	2001US-0305366P.	
PR	(PION-) PIONEER HI-BRED INT INC.		
XX	Navarro Acevedo PA, Duvick JP, Kolomiets MV, Simmons CR;		
PI	WPI; 2003-898106/82.		
XX	N-PSDB; ADG93386.		
DR	New lipoxigenase polypeptides and polynucleotides, useful for enhancing		
PT	resistance to pathogens, e.g. fungi, viruses, nematodes or insects, for		
PT	promoting healing of damage tissues, or for modulating plant growth and		
PT	development.		
XX	Claim 1; SEQ ID NO 18; 151pp; English.		
PS	The invention relates to maize lipoxigenase (LOX) polypeptides and		
XX	polynucleotides encoding the polypeptides. The LOX polypeptides and		
CC	polynucleotides are useful in modulating plant pathogen defence systems		
CC	(particularly enhancing resistance to fungi, viruses, nematodes and		
CC	insects) and plant development, and for promoting healing of damaged		
CC	tissues. LOX proteins may also be used to inhibit the production of		
CC	mycotoxins of fungi (e.g. aflatoxin) and sterigmatocystin producing		
CC	fungus in plants susceptible to contamination by the mycotoxins. This		
CC	sequence represents a maize LOX polypeptide of the invention.		
XX	Sequence 887 AA;		
SQ	Query Match	60.3%;	Score 2734.5; DB 7; Length 887;
	Best Local Similarity	59.6%;	Pred. No. 9.4e-227;
	Matches	530; Conservative	115; Mismatches 214; Indels 31; Gaps 11;
QY	1	MFLEKIVDAITGKD----	DGKKVKGTVVLMKKNVLDFTDINASVLDGVLEFLG--RRVSL 54
Db	1	MFHWGVADRLTGKNKEAWNEGKIRGTVRLVKEVLDVGDFNASLLDGVHRLGWDDGVAF	60
QY	55	ELISSVNADPANGLOQKRSKAAAYLENWLTNSTPIAAGESAFRVTFDWDEEFGVPGAFII	114
Db	61	QLVSATAADPSNGSRGKVGKAAHLEAAVSLKSTTDGETVYRVVSFEWDGSQ-GVPGAVLV	119
QY	115	KNLHSEFFFLKSLTLEDVPHNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLR	174
Db	120	RNLQHAEFFFLKSLTLEGVPGRGTVVFVANSWIYPHNLYSQERVFVFANDTYLPSKMPAALV	179
QY	175	KYRENELVTLRG-DGTGKLEEWDRVYDYAYYNDLGDPPDKQDLSRPPVLGGSSEYPYPRRG	233
Db	180	PYRQDELKILRGDDNPGPYKEHDRVYDYNDLGEPPDKGEDHARPVLGGSQEHYPYPRRC	239
QY	234	RTGRKPTKTDPNSESRIPLMLSLDIYVPRDERFGHIKLSDFLTFAKLSIVQLLPEFKAL	293
Db	240	RTGRRPTETDPNSESRL-FLNLNIIYVPRDERFGHLKMSDFLGYSLKAIIEAVLPTLGRF	298
QY	294	FDSTHNEFDSFEDVLKLYEGGIKLPQGILLKAITDSIPLEILKELLRSDG--EGLFKYPT	351
Db	299	VDDTPKEFDSFEDILGLYEPGPEAPNPNPLVAEVRKRIPISEFLRSIL-PDGSHDHPLKMPL	357
QY	352	PQVIQED-----KTAWRTDEEFGREMLAGVNPVVISRLQEPFPKSKLDPKIYGNQNS	403
Db	358	PNIIRSDVLKKAPEFKFGWRTDEEFARETLAGVNPVLIKRLTEFFPAKSTLDPSQYGDHTS	417
QY	404	TITREQIEDKLDGLTIDEAIKTNRLFILNHHDIILMPYLRRINTSTDTKTYASRTLLFLQD	463
Db	418	KITEAHIQHNMEGLSVQNALKKNRFLILDHHDHFMPLYLNKINELEGNFIYASRTLLFLKD	477
QY	464	NGTLKPSAIELSLPHPDGQFGAVSKVYTPADQGVGSIWQLAKAYAAVNDSGVHQLISH	523
Db	478	DGTLKPLAVELSLPHPDGQGHGAVSKVYTPAHSGAEGHVWQLAKAYACVNDSAWHQLISH	537
QY	524	WLNTHAAIEPFFVIATNRQLSALHPYIKLLHPHFRETMINALARQILINGGGLLELTVFP	583





Db 778 TITSQFQTLGISLIEILSKHSSDEVYLGQRDEPDRWTSDAKALDAFKRFGSRLVQIENR 837  
Qy 820 IMQMNVDKWKNRSGPVKVPYTLFFPTSEG-----GLTGKIPNSVSI 862  
Db 838 IKTWNDSDDLKNRKGPVEMPYMLLYPNTSDVTGEKAEGLTAMGIPNSISI 887

Search completed: March 10, 2005, 18:59:00  
Job time : 186 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 10, 2005, 18:56:07 ; Search time 149 Seconds  
(without alignments)  
1908.230 Million cell updates/sec

Title: US-10-731-642A-1  
Perfect score: 4534  
Sequence: 1 MFLEKIIVDAITGKDDGKVK.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3610	79.6	859	10	US-09-978-522-3
2	3576	78.9	862	10	US-09-978-522-1
3	3346.5	73.8	887	15	US-10-425-114-54449
4	3104.5	68.5	864	15	US-10-425-114-46828
5	3090	68.2	859	15	US-10-424-599-213159
6	3022.5	66.7	880	14	US-10-059-909-12
7	2909	64.2	857	15	US-10-424-599-215976
8	2909	64.2	860	15	US-10-425-114-45769
9	2909	64.2	863	15	US-10-425-114-54429
10	2909	64.2	863	15	US-10-425-114-55253
11	2905	64.1	857	10	US-09-751-687-17
12	2849.5	62.8	826	15	US-10-424-599-215973
13	2849.5	62.8	832	15	US-10-425-114-45631

14	2791.5	61.6	888	16	US-10-437-963-165232	Sequence 165232,
15	2790	61.5	860	15	US-10-424-599-220216	Sequence 220216,
16	2769.5	61.1	864	14	US-10-132-350-10	Sequence 10, Appl
17	2769.5	61.1	864	14	US-10-132-350-12	Sequence 12, Appl
18	2763.5	61.0	871	15	US-10-425-114-62385	Sequence 62385, A
19	2755.5	60.8	865	15	US-10-424-599-258944	Sequence 258944,
20	2754	60.7	866	15	US-10-424-599-239573	Sequence 239573,
21	2745.5	60.6	865	10	US-09-751-687-16	Sequence 16, Appl
22	2734.5	60.3	887	14	US-10-132-350-18	Sequence 18, Appl
23	2734.5	60.3	887	14	US-10-132-350-20	Sequence 20, Appl
24	2733.5	60.3	926	15	US-10-425-114-69756	Sequence 69756, A
25	2730.5	60.2	866	16	US-10-437-963-116093	Sequence 116093,
26	2727	60.1	786	15	US-10-425-114-46295	Sequence 46295, A
27	2724.5	60.1	887	14	US-10-059-909-16	Sequence 16, Appl
28	2724.5	60.1	887	14	US-10-132-350-22	Sequence 22, Appl
29	2724.5	60.1	887	14	US-10-132-350-24	Sequence 24, Appl
30	2704	59.6	881	15	US-10-425-114-57754	Sequence 57754, A
31	2704	59.6	964	16	US-10-425-114-54555	Sequence 54555, A
32	2704	59.6	964	16	US-10-437-963-141895	Sequence 141895,
33	2700.5	59.6	873	14	US-10-132-350-2	Sequence 2, Appli
34	2700.5	59.6	873	14	US-10-132-350-4	Sequence 4, Appli
35	2700.5	59.6	891	15	US-10-425-114-62915	Sequence 62915, A
36	2700	59.6	868	15	US-10-424-599-242598	Sequence 242598,
37	2699	59.5	856	15	US-10-424-599-151512	Sequence 151512,
38	2694.5	59.4	853	15	US-10-424-599-151510	Sequence 151510,
39	2694.5	59.4	860	15	US-10-425-114-39867	Sequence 39867, A
40	2694.5	59.4	862	15	US-10-425-114-42418	Sequence 42418, A
41	2694.5	59.4	863	15	US-10-425-114-39883	Sequence 39883, A
42	2694.5	59.4	863	15	US-10-425-114-47348	Sequence 47348, A
43	2694.5	59.4	865	15	US-10-425-114-40151	Sequence 40151, A
44	2694.5	59.4	866	15	US-10-425-114-40047	Sequence 40047, A
45	2694.5	59.4	867	15	US-10-425-114-39889	Sequence 39889, A

ALIGNMENTS

RESULT 1  
US-09-978-522-3  
; Sequence 3, Application US/09978522  
; Publication No. US20030033627A1  
; GENERAL INFORMATION:  
; APPLICANT: Descenzo, Richard  
; APPLICANT: Ireland, Nancy  
; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera  
; FILE REFERENCE: 29520/37890  
; CURRENT APPLICATION NUMBER: US/09/978,522  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 60/241,220  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 859  
; TYPE: PRT  
; ORGANISM: Vitis LOX 2  
US-09-978-522-3

Query Match	79.6%;	Score 3610;	DB 10;	Length 859;
Best Local Similarity	76.9%;	Pred. No. 1.3e-285;		
Matches	661;	Conservative 106;	Mismatches 91;	Indels 2; Gaps 2;
Qy	3	LEKIVDAITGKDDGKKVKTGTVLMKKNVLDFTDINASVLDGVLEFLGRRVSLLEISSVNA	62	
Db	2	IHSIVGAITGENDKKIKGTIVLMKKNVLDNFDFNASVLDRVHLLGQGVPLQLVSAVHG	61	
Qy	63	DPANGLQCKRSKAAYLENLWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHFSEF	122	
Db	62	DPANGLQCKIGKPAYLEDWITTTSLTAGESAFKVTFDW-DEEIGEPGAFIIRNNHSEF	120	
Qy	123	FLKSLTLEDVPHGKVFVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELV	182	
Db	121	YLRTLTLEDVPGRIHFVCNSWVYPAHQYKTDTRVFTTQTYLPSETPGPLRKYREGELV	180	











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Query Match      66.7%; Score 3022.5; DB 14; Length 880;
Best Local Similarity 65.4%; Pred. No. 1.4e-237;
Matches 554; Conservative 132; Mismatches 156; Indels 5; Gaps 4;

QY 16 GKKVKGTVVLMKKNVLDFTDINASVLGDVLEFLGRVSVLELISSVNADPANGLOQKRSKA 75
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 39 GKKIKGTVLMRSNVLDFTFTHSSLLDGVTELLGGGISLQLISATHA--SNDGRGKVGGK 96

QY 76 AYLENWLTNSTPIAAGESAPRVTFDWDDEEFGVPGAFIIKNLHFSEFFLKSLTLEDVPNH 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 97 AFLERWLTSVPLFAGESVFQVNFWDW-EENFGFPGAFIKNIGHTSEFFLKSVTLEDVPGF 155

QY 136 GKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYRENELVTLRGDGTGLEEW 195
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 156 GRVHFDNCWVPSRRYKKDRIFFAHTCLPIDTPDSLRYKREELNLNRGDGTGERKEW 215

QY 196 DRVYDYAYNDLGDPPKQDLSRPVLGSGSEYPPYPRGRGTGRKPTKTDPNSESRIPLMS 255
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 216 DRIYDYDVNDLCDPNGGPNLVRPILGSDQYPPRRGRGTGRPPARKDHYESRLSDVMS 275

QY 256 LDIYVPRDERFGHIKLSDFLTALKSIVQLLPEFKALFDSHNEFFDSFEDVLKLYEGGI 315
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 276 LNIYVPRDENFGHLKNADFLGNTLKVLSSTIQGLSIFDSTPGEFFDKFEVDDLFERGF 335

QY 316 KLPQGPLLKAITDSIPLEILKELLRSDDGEGFLKYPTPQVIOEDKTAWRTDEEFGREMLAG 375
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 336 PIPLN-IFKNLTDLAPPLFAFLRSDDGERFLKYPTPQVIKONKLGWRTDEFAREMIAG 394

QY 376 VNPVIISRLQEFFPKSKLDPKIYGNQNSTITREQIEDKLDGLTIDEAIKTNRLFILNHH 435
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 395 VNPLIIRLEVPPLSKLDPHVYGNQNSTWTEEQIKHGLDGLTVDEAIKENKLYILDHHD 454

QY 436 ILMPYLRRINTSTDTKTYASRTLFLQDNGTLKPSAIELSLPHPDGDQFGAVSKVYTPAD 495
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 455 ALMPYLRRIN-STSTKYATRTLFLKDDSTLKLPLAIELSLPHPQGDGEGHGAISKLYPAE 513

QY 496 QGVEGSIWOLAKAAVAVNDSGVHQLISHWLNTTHAAIEPFVVIATNRQLSALHPIYKLLHPH 555
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 514 GRVESAIWOLAKAAVAVNDSGYHQLNSHWLTHAVLEPFVITTHRRLSVLHPHKLAPH 573

QY 556 FRETMINALARQILINGGGLLELTVFPKAYSMEMSAVVYKDWVFPPEQALPTDLIKRGVA 615
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 574 YKOTMFINASARQVLINAGGLIESTQFPKAYAMELSSYIYKEWKFPDEALPTNLIKRGVA 633

QY 616 VEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKSDDAVQKDTQLQAWWKE 675
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 634 IEDSGSPHGVRLINDYPFAVDGLEIWSAIKTWVTDYCSLYKODDAIRNDVELQSWWKE 693

QY 676 LREEGHGDKKDEPWPMPKMTVQELIDSCITITTIWIASALHAAVNFQYYPYAGVLPNRP 735
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 694 LREKGTDKKDEPWPMPKMTFSELIESCTIIIIWISSALHAAVNFQYYPYGGVYVNP 753

QY 736 RNFMPEPGSPEYEELKTNPDKVFLKTTITPQLQTLIGISLIEILSRHSSDTLYLGQRESPE 795
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 754 RRFMEVGTAEYKEVESNPEKAFLRTISSQIVALLGLSIIELSKHASDEVYLGORASIE 813

QY 796 WTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPVKVPYTYLLFPTSEGGLTGKG 855
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 814 WTSDKSAIEAFEKFGKELFEVEDRIMRRNQDVLNKNRAGPVNMPYTYLLVPSSTEGLTGRG 873

QY 856 IPNSVSI 862
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Db 874 IPNSISI 880
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RESULT 7  
US-10-424-599-215976  
; Sequence 215976, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K

```
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215976
; LENGTH: 857
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37056C.1.pep
US-10-424-599-215976
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Query Match      64.2%; Score 2909; DB 15; Length 857;
Best Local Similarity 63.4%; Pred. No. 2.6e-228;
Matches 549; Conservative 122; Mismatches 159; Indels 36; Gaps 9;

QY 16 GKKVKGTVVLMKKNVLDFT-----DINASVLGDVLEFLGRVSVLELISSVNA 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 GHKIKGTVLMRKKNVLDVNSVTSVGGIIGQGLDLVGSLDTLTFLGRSVSLQLISATKA 68

QY 63 DPANGLQGRSKAAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHFSEF 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 D-ANG-KGKLGKATFLEGIITSLPTLGAGQSAPKINFWDGGS-GIPGAFYIKNFMQTEF 125

QY 123 FLKSLTLEDVPHGKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYRENELV 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 126 FLVSLTLEDIPNHGSIHFVCNSWIYNAKLFPKSDRIFFANQTYLPSETPAPLVKYREEELH 185

QY 183 TLRGDGTGLEEWDVRVYDYAYNDLGDPPKQDLSRPVLGSGSEYPPYPRGRGTGRKPTKT 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 186 NLRGDGTGERKEWERIYDYDVNDLGDPPDKGENHARPVLGGNDTFPPYPRGRGTGRKPTRK 245

QY 243 DPNSESRIPLMSLDIYVPRDERFGHIKLSDFLTALKSIVQLLPEFKALFD--STHNE 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 246 DPNSESR-----SNDVYLPRDEAFGHLKSSDFLTYGLKSVSQNVLPQLQSAFDLNFPTPRE 300

QY 301 FDSFEDVLKLYEGGIKLPQGPLLKAITDSI----PLEILKELLRSDDGEGFLKYPTPQV 356
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 FDSFDEVHGLYSGGIKLP-----TDIISKISPLPVLKEIFRTDGEQALKFPPPKV 352

QY 357 EDKTAWRTDEEFGREMLAGVNPVVIISRLQEFFPKSKLDPKIYGNQNSTITREQIEDKLDG 416
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 353 VKSAAWMTDEEFAREMLAGVNPNLIRCLKDFPPRSKLDQVYGDHTSQITKEHLEPNLEG 412

QY 417 LTIDEAIKTNRLFILNHHDLMPYLRRINTSTDTKTYASRTLFLQDNGTLKPSAIELSL 476
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 413 LTVDEAIQNKRDLFLLDHHDPIMPYLRRIN-ATSTKAYATRITLFLKNDGTLRPLAIELSL 471

QY 477 PHPDGDQFGAVSKVYTPADQGVESIWOLAKAAVAVNDSGVHQLISHWLNTTHAAIEPFVI 536
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 472 PHPQGDQSGAFSQVFLPADEGVESIWLLAKAYVAVVNDSCYHQLVSHWLNTTHAVVEPFI 531

QY 537 ATNRQLSALHPIYKLLHPHFRETMINALARQILINGGGLLELTVFPKAYSMEMSAVVYK 596
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 532 ATNRHLSVVHPIYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTFLWGRYSVEMSAVVYK 591

QY 597 DWVFPEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYY 656
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 592 DWVFTDQALPADLIKRGMAIEDPSCPHGIRLVIEDYPYAVDGLEIWDIAIKTWVHEYVFLY 651

QY 657 YKSDDAVQKDTQLQAWWKELREEGHGDKKDEPWPMPKMTVQELIDSCITITTIWIASALHAA 716
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 652 YKSDDTLREDEPELQACWKELVEVGHGDKKNPWPMPKMTREELVEACAIITWASALHAA 711

QY 717 VNFQGYPYAGVLPNRPRTLNRNFMPEPGSPEYEELKTNPDKVFLKTTITPQLQTLIGISLIE 776
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 712 VNFQGYPYGGLILNRPRTLRRRFPMPKESAEYEELRKNPQKAYLKTITPKFQTLIDLVSIE 771

QY 777 ILSRHSSDTLYLGQRESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPV 836
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Db 772 ILSR HASDEVYLGERDNPNTSDTRALEAFKFGNKLQAIENKLSERNNDKLRNRCGPV 831

QY 837 KVPYTLTFPTSEGGLTGKGPNSVSI 862

Db 832 QMPYTLTLLPSSKEGLTFRGIPNSISI 857

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RESULT 8
US-10-425-114-45769
; Sequence 45769, Application US/10425114
; Publication NO. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45769
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700675903_FLI.pep
US-10-425-114-45769

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	Query Match	64.2%;	Score 2909;	DB 15;	Length 860;
	Best Local Similarity	63.4%;	Pred. No. 2.6e-228;		
	Matches 549;	Conservative 122;	Mismatches 159;	Indels 36;	Gaps 9;
QY	16	GKKVKGTVLMMKNVLDFT-----DINASVLDGVLEFLGRRVLSLELISSVNA	62		
DB	12	GHKIKGTVLMRKNVLDVNSVTSVGIIQGQLDVGSLDTLTAFLGRSVSLQISATKA	71		
QY	63	DPANGLQGRSKAAAYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIINKLHFSEF	122		
DB	72	D-ANG-KGKLGKATFLEGIITSLPTLGAGQSFAKINFEWDDGS-GIPGAFYIKNFMQTEF	128		
QY	123	FLKSLTLEDVPNHGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELV	182		
DB	129	FLVSLTLEDIPNHGSIHFVCNSWIYNAKLFKSDRIFFANQTYLPSETPAPLVKYREELH	188		
QY	183	TLRGDGTGKLEEDRVVDYAYNDLGDGDPKQDLSRPLVIGSSEYYPYPRRGRTGRKPTKT	242		
DB	189	NLRGDGTGERKEWERIYDYVDYNDLGDGDPKGENHARPVLGNDTFYPYPRRGRTGRKPTRK	248		
QY	243	DPNSESRIPLMLSDIYVPRDERFPGHIKLSDFLTFALKSIVQLLLPEFKALFD--STHNE	300		
DB	249	DPNSESRIPLMLSDIYVPRDERFPGHIKLSDFLTFALKSIVQLLLPEFKALFD--STHNE	303		
QY	301	FDSFEDVLKLYEGGIKLPGQPLLKAITDSI----PLEILKELLRSDEGLFKYPTPQVIQ	356		
DB	304	FDSFDEVLKLYEGGIKLPGQPLLKAITDSI----PLEILKELLRSDEGLFKYPTPQVIQ	355		
QY	357	EDKTAWRTDEEFGREMLAGVNPVVISRLQEFPPKSKLPDKTYGNQNSTITREQIEDKLDG	416		
DB	356	VKSAAWMTDEEFAREMLAGVNPVNLIRCLKDFPPRSKLDQVYGDHTSQITKEHLEPNLEG	415		
QY	417	LTIDEAICTNRRLFILNHHDIIMPYLRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSL	476		
DB	416	LTVDEAIQNKRLFLDDHDDPIMPYLRIN-ATSTKAYATRTILFLKNDGTGLRPLAIELSL	474		
QY	477	PHPDGDQFGAVSKVYTPADQGVGSGIWQLAKAYAAVNDSGVHQLISHWLNTTHAAIEPFVI	536		
DB	475	PHPOGDOSGAFSQVFLPADQGVGSGIWQLAKAYAAVNDSCYHQLVSHWLNTTHAVPEPFI	534		

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Qy 537 ATNRQLSALHPYIKLLPHFRETWNINALARQILINGGGLLELTVFPKAYMEMSAVYK 596
Db 535 ATNRHLSVVHPYIKLLPHFYRDTMNINGLARLSLVNDGGVIEQTFLWGRYSVEMSAVYK 594
Qy 597 DWVFPEQALPTDLTKRGVAVEDSSSPGLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNY 656
Db 595 DWVFTDQALPADLIKRGMAIEDPSCPHGIRLVIEDYPYAVDGLGIWDIAKTWVHEYVPLY 654
Qy 657 YKSDDAVQKDTELQAWWKELREEGHGDKDEPPWPKMQTVQELIDSCITIIWIASALHAA 716
Db 655 YKSDDTLREDPELOACWKELVEVGHDKKNEPWWPKMQTREELVEACAIIWTASALHAA 714
Qy 717 VNFQOYPYAGYLNPRTLRSNFMPEPGSPYEELKTNPNKVFLKITTPOLQTLGISLIE 776
Db 715 VNFQOYPYGGLINRPRTLRRFMPEKGSABEELRNKPQKAYLKITTPKFOTLIDLVSIE 774
Qy 777 ILSRHSSDTLYLGRESPEWTKDOEPLSAFAFRFGKLSIDIOIMQMNVDKWKNRSGPV 836
Db 775 ILSRHASDEVYLGDRDNPNWTS DTRALEAFKRFGNKLAQIENKLSENNDEKLNRCCGPV 834
Qy 837 KVPYTLLFPTSEGGLTGKIPNSVSI 862
Db 835 QMPYTLLLPSSKEGLTFRGIPNSISI 860

RESULT 9
US-10-425-114-54429
; Sequence 54429, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54429
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700842448_FLI.pep
US-10-425-114-54429

Query Match          64.2%; Score 2909; DB 15; Length 863;
Best Local Similarity 63.4%; Pred. No. 2.6e-228;
Matches 549; Conservative 122; Mismatches 159; Indels 36; Gaps 9;

Qy 16 GRKVKGTVMKKNVLDF-----DINASVLGDVLEFLGRRVSLIELISSVNA 62
Db 15 GHKIKGTVMRMKNVLDVNSVTSGGIQGGLDLVGSTLDTLTAFLGRSVSLQLISATKA 74
Qy 63 DPANGLQKRSKAAYLENLWLTNSTPIAAGESAFRVTFDWDEEGVPGAFIINKLHFSEF 122
Db 75 D-ANG-KGKLGKATFLEGIITSLPTLAGQSFAKINFEDDGS-GIPGAFYIKNFMQTEF 131
Qy 123 FLKSLTLEDVFNHGKHVFCNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKXYRENELV 182
Db 132 FLVSLTLEDIPNHGSHIFVCNSWIYNAKLFKSDRIFFANQTYLFPSETPAPLVKYREELH 191
Qy 183 TURGDGTGLEEWRVDYDAYYNDLGDPPDKQDLSRPVLGGSSEYPYPRRGRTRGKPKTK 242
Db 192 NLRGDGTGERKEWERIYDYDVYNDLGDPPDKGENHARPVLGGNDTFPYPRRGRTRGKPKTRK 251
Qy 243 DPNSERIPLLMSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLPEFKALFD--STHNE 300
Db 252 DPNSER-----SNDVYLPDRDEAFGLKSSDELTYGLKSVSONVLP LLQSAFDLNFPTPRE 306

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; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 857  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-751-687-17

Query Match 64.1%; Score 2905; DB 10; Length 857;  
Best Local Similarity 63.3%; Pred. No. 5.5e-228;  
Matches 548; Conservative 122; Mismatches 160; Indels 36; Gaps 9;

Qy	16	GKKVKGTVVLMKKNVLDFT-----DINASVLDGVLEFLGRRVSLLELISSVNA	62
Db	9	GHKIKGTVVMRKNVLDVNSVTSVGGIIGQLDLVGLSTLDTLTAFLGRSVSLQISATKA	68
Qy	63	DPANGLOGKRSKAAYLENWLTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFSEF	122
Db	69	D-ANG-KGKLGKATFLEGIITSLPTLGAGQSAFKINFWDGSG-GIPGAFYIKNFMQTEF	125
Qy	123	FLKSLTLEDVPHGKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELV	182
Db	126	FLVSLTLEDIPNHGSIHFVCNSWIYNAKLFKSDRIFFANQTYLPSETPAPLVKYREEELH	185
Qy	183	TLRGDGTGKLEEDRVYDYAYNDLGDPPDKQDLRSPVLGGSSEYPPRRGRTGRKPKTK	242
Db	186	NLRGDGTGERKEWERIYDYDVYNDLGDPPDKGENHARPVLGGNDTFPPRRGRTGRKPKRK	245
Qy	243	DPNSESRIPLLMSLDIYVPRDERFHHIKLSDFLTALKSIVQLLLPEFKALFD--STHNE	300
Db	246	DPNSES-----SNDVYLPRDEAFGHLKSSDFLTGYLKSVSQNVLPQLQSAFDLNFPTRE	300
Qy	301	FDSFEDVLKYEGGIKLPQGPLLKAITDSI-----PLEILKELLRSDDGGLFKYPTPOVIO	356
Db	301	FDSFDEVHGLYGGIKLP-----TDIISKISPLPVLKEIFRTDGEQALKFPPPKVIO	352
Qy	357	EDKTAWRTDEEFGREMLAGVNPVIISRLQEFPPKSKLPKIYGNQNSTITREQIEDKLDG	416
Db	353	VKSAMWTDDEFAREMLAGVNPNLIRCLKDFPPRSKLDQVYGDHTSQITKEHLEPNLEG	412
Qy	417	LTIDEAIAKTNRLFILNHHDIIMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSL	476
Db	413	LTVDEAIONKRLFLLDHHDPIMPYLRRIN-ATSTKAYATRILFLKNDGTLRPLAIELSL	471
Qy	477	PHPDGDQFQAVSKVYTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTAAIEPFI	536
Db	472	PHPQDQSGAFSQVFLPADEGVESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFI	531
Qy	537	ATNRQLSALHPIYKLLHPHFRETMTNINALARQILINGGGLLELTVFPKYSMEMSAVVYK	596
Db	532	ATNRHLSVVHPIYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTLWGRYSVEMSAVVYK	591
Qy	597	DWVFPEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNVY	656
Db	592	DWVFTDQALPADLIKRGMAIEDPSCPHGIRLVIEDYPYTVDGLIWDIAIKTWHEYVFLY	651
Qy	657	YKSDDAVQKDTELQAWWKELREEGHGDKDEPWPMPKMTVQELIDSCITITWIASALHAA	716
Db	652	YKSDDTLREDPELOACWKELVEVGHGDKNEPWPMPKMTREELVEACAIITWASALHAA	711
Qy	717	VNFGQYPYAGYLPNRPRTLNRNFMPEPGSPYEEELKTNPDKVFLLKTIIPQLOTLGLISLIE	776
Db	712	VNFGQYPYGGIILNRPRTLNRFRFMEKGSABEELRNKPQKAYLKTITPKFQTLIDLVSIE	771
Qy	777	ILSRHSDTLYLGQRESPEWTKDQEPISAFARFGKLSDIEDQIMQNVNDEKWNRSRGPV	836
Db	772	ILSRHASDEVYLGERNPNWTSDTTRALEAFKRFNGKLAQIENKLSENNDEKLRNRCGPV	831
Qy	837	KVPYTLFFTSBEGGLTGKIPNSVSI	862
Db	832	QMPYTLPLPSKEGLTFRGIPNSISI	857

RESULT 12  
US-10-424-599-215973  
; Sequence 215973, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 215973  
; LENGTH: 826  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_37053C.1.pap  
US-10-424-599-215973

Query Match 62.8%; Score 2849.5; DB 15; Length 826;  
Best Local Similarity 62.7%; Pred. No. 1.8e-223;  
Matches 535; Conservative 122; Mismatches 155; Indels 41; Gaps 9;

Qy	16	GKKVKGTVVLMKKNVLDFTDINASVLDGVLEFLGRRVSLLELISSVNDPANGLOGKRSKA	75
Db	9	GHKIKGTVVMRKNVLDVNSVTS--VGGII-----GQANG-KGKLGKA	48
Qy	76	AYLENWLTNSTPIAAGESAFRVTFDWDDEFGVPGAFIKNLHFSEFFLKSLTLEDVPHN	135
Db	49	TFLEGIITSLPTLGAGQSAFKINFWDGSG-GIPGAFYIKNFMQTEFFLVSLTLEDIPNH	107
Qy	136	GKVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPDTLRKYRENELVTLRGDGTGKLEEW	195
Db	108	GSIHFVCNSWIYNAKLFKSDRIFFANQTYLPSETPAPLVKYREEELHNLRGDGTGERKEW	167
Qy	196	DRVYDYAYNDLGDPPDKQDLRSPVLGGSSEYPPRRGRTGRKPKTKTDPNSESRIPLMS	255
Db	168	ERIYDYDVYNDLGDPPDKGENHARPVLGGNDTFPPRRGRTGRKPKTRKDPNSES	222
Qy	256	LDIYVPRDERFHHIKLSDFLTALKSIVQLLLPEFKALFD--STHNEFDSFEDVLKLYEG	313
Db	223	NDVYLPRDEAFGHLKSSDFLTGYLKSVSQNVLPQLQSAFDLNFPTREFDSFDEVHGLYSG	282
Qy	314	GIKLPQGPLLKAITDSI-----PLEILKELLRSDDGGLFKYPTPOVIEDKTAWRTDEEFG	369
Db	283	GIKLP-----TDIISKISPLPVLKEIFRTDGEQALKFPPPKVIOVSKSAWMTDEEFA	334
Qy	370	REMLAGVNPVIISRLQEFPPKSKLPKIYGNQNSTITREQIEDKLDGLTIDEAIAKTNRLF	429
Db	335	REMLAGVNPNLIRCLKEFFPPRSKLDQVYGDHTSQITKEHLEPNLEGLTVDEAIONKRLF	394
Qy	430	ILNHHDIIMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPDGDQFQAVSK	489
Db	395	LLDHHDPIMPYLRRIN-ATSTKAYATRILFLKNDGTLRPLAIELSLPHPDQDQSGAFSQ	453
Qy	490	VYTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTAAIEPFIATNRQLSALHPIY	549
Db	454	VFLPADEGVESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFIATNRHLSVVHPIY	513
Qy	550	KLLHPHFRETMTNINALARQILINGGGLLELTVFPKYSMEMSAVVYKDWVFPEQALPTDL	609
Db	514	KLLHPHYRDTMNINGLARLSLVNDGGVIEQTLWGRYSVEMSAVVYKDWVFTDQALPADL	573
Qy	610	IKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAISKSWVTEYCNYYKSDDAVQKDTEL	669
Db	574	IKRGMAIEDPSCPHGIRLVIEDYPYAVDGLIWDIAIKTWHEYVFLYKSDDTLREDPEL	633
Qy	670	QAWWKELREEGHGDKDEPWPMPKMTVQELIDSCITITWIASALHAAVNFQYPYAGYLP	729

Db 634 QACWKELVEVGHGDKKNEPWPVKMQTREELVEACAIITWTASALHAAVNFQGPYGGIL 693

QY 730 NRPTLSRNFMPGSPYEELKTNPKVFLKTIITPQLTLLGISLIEILSRHSDTLYLG 789

Db 694 NRPTLSRRFMPEKSAEYELRNPKQAYLKTITPKFQTLIDLSVIEILSRHASDEVYLG 753

QY 790 QRESPEWTKDQEPISAFARFGKLSIEDIQIMQNVDEKWKNSRGPVKPYTLLFPTSEG 849

Db 754 ERDNPNTSDTRALEAFKFRGNKLAQIENKLSERNNDEKLRNRCGPVQMPYTLLLPSSKE 813

QY 850 GLTGKGIPNSVSI 862

Db 814 GLTFRGIPNSISI 826

RESULT 13

US-10-425-114-45631

; Sequence 45631, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 45631

; LENGTH: 832

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: 700733503\_FLI.pep

US-10-425-114-45631

Query Match 62.8%; Score 2849.5; DB 15; Length 832;

Best Local Similarity 62.7%; Pred. No. 1.8e-223;

Matches 535; Conservative 122; Mismatches 155; Indels 41; Gaps 9;

QY 16 GKVKGTIVLMKKNVLDFTDINASVLGDGVLEFLGRRVLSLELISSVNADPANGLOGKRSKA 75.

Db 15 GHKIKGTIVLMKKNVLDVNSVTS--VGGII-----GQANG-KGKLGKA 54

QY 76 AYLENWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHFSEFFLKSLTLEDVPH 135

Db 55 TFLEGIITSLPTLGAGQSAFKINFEWDDGS-GIPGAFYIKNFMQTEFFLVSLTLEDIPNH 113

QY 136 KGVHFCVNSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYRENELVTLRGDGTGKLEEW 195

Db 114 GSIHFVCNSWIYNAKLFKSDRIFFANQTYLPSETPAPLVKYREEELHNLRLRGDTGERKEW 173

QY 196 DRVYDYAYNDLGDGQDLRSRVLGGSSEYPYPRRGRTGRKPTKTDPNSESRIPLLMS 255

Db 174 ERIYDYDVNDLGDGPKGENHARPVLGNDTFYPRRGRTGRKPTRKDENSER-----S 228

QY 256 LDYVPRDERFHHKLSDFLTALKSIVQLLPEFKALFD--STHNEFDSFEDVLKLYEG 313

Db 229 NDVYLPRDEAFGHLKSSDFLTGLKSVSONVPLLLQSAFDLNFTPREFDSFDEVHGLYSG 288

QY 314 GIKLPQGPLLKAITDSI----PLEILKELLRSDGEGLFKYPTPQVIQEDKTAWRTDEEFG 369

Db 289 GIKLP-----TDIISKISPLVPLKEIFRTDGEQALKFPPPKVIOVKSAMWMTDEEFA 340

QY 370 REMLAGVNPVITSRLOQFPPKSLDKPKIYGNQNSTITREQIEDKLDGLTIDEAICTNRLF 429

Db 341 REMLAGVNPNLIRCLKEFPFRSKLDSQVYGDHTSQITKEHLEPNLEGLTVDEAIQNKRLF 400

QY 430 ILNHHDILMPYLRRINTSTDTKTYASRTLLFLQDNGTLKPSAIELSLPHPDGDQFGAVSK 489

Db 401 LLDHHDIMPYLRRIN-ATSTKAYATRTILFLKNDGTLRLPLAIELSLPHPDGQSGAFSQ 459

QY 490 VYTPADQGVESIWQLAKAYAAVNDSGVHQLISHWLNTHAAIEPFVIATNRQLSALHPIY 549

Db 460 VFLPADEGVESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFIATNRHLSVVHPIY 519

QY 550 KLLHPHFRETMINALARQILINGGGLLELTVFPKAYKSMEMSAVVYKDWVPFEQALPTDL 609

Db 520 KLLHPHYRDTMNINGLARLSLVNDGGVIEQTLWGRYSVEMSAVVYKDWVFTDQALPADL 579

QY 610 IKRGVAVEDSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKSDDAVQKDTL 669

Db 580 IKRGMAIEDPSPGHGIRLVIEDYPYAVDGLIWDIAIKTWHEYVFLYKSDDTLREDPEL 639

QY 670 QAWWKELREEGHGDKKDEPWPVKMQTVQELIDSCITITWIASALHAAVNFQGPYAGYLP 729

Db 640 QACWKELVEVGHGDKKNEPWPVKMQTREELVEACAIITWTASALHAAVNFQGPYGGIL 699

QY 730 NRPTLSRNFMPGSPYEELKTNPKVFLKTIITPQLTLLGISLIEILSRHSDTLYLG 789

Db 700 NRPTLSRRFMPEKSAEYELRNPKQAYLKTITPKFQTLIDLSVIEILSRHASDEVYLG 759

QY 790 QRESPEWTKDQEPISAFARFGKLSIEDIQIMQNVDEKWKNSRGPVKPYTLLFPTSEG 849

Db 760 ERDNPNTSDTRALEAFKFRGNKLAQIENKLSERNNDEKLRNRCGPVQMPYTLLLPSSKE 819

QY 850 GLTGKGIPNSVSI 862

Db 820 GLTFRGIPNSISI 832

RESULT 14

US-10-437-963-165232

; Sequence 165232, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 165232

; LENGTH: 888

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_64058C.1.pep

US-10-437-963-165232

Query Match 61.6%; Score 2791.5; DB 16; Length 888;

Best Local Similarity 61.2%; Pred. No. 1.1e-218;

Matches 534; Conservative 120; Mismatches 198; Indels 21; Gaps 8;

QY 8 DAITGKD----DGKKVKGTIVLMKKNVLDFTDINASVLGDGVLEFLGRR--VSLELISSV 60

Db 19 DRLTGRNKEAWKEG-RIRGTAVLVKKDVLGLGDFHASLLDGVHNLHGKEGVAFRLVSAT 77

QY 61 NADPANGLOGKRSKAAYLENLWLTNSTPIAAGESAFRVTFDWDDEEFGVPGAFIKNLHFS 120

Db 78 ARDPSNGRGKLGKPAHLEELVVTMKSTAAGESVFRVAFEWDESQ-GIPGAVVVTNSRS 136

QY 121 EFFLKSILTLEDVPHGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYRENE 180

Db 137 EFFLKTLDGVPKGTVFVANSWIYPADNYQYERVFFANDTYLPSKMPAPLIPYRQEE 196

QY 181 LVTLRGDG-TGKLEEDRWVDYAYVNDLGDGDPKQDLSRPVLGSGSEYPYPRRGRTGRKP 239

Db 197 LNILRGDGKIGPYKEHDRIYRYDYNDLGQDPDKGSLVRPVLGSGQELPYPRRGRTGRAP 256

QY 240 TKTDPNSESRIPLIMSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLLPEFKALFDSTHN 299

Db 257 TKTDPNTESRLPLL-DLNIYVPRDERFGHLKMSDFLGYSLKAIVEGVLPPIIRTYVDTPK 315

QY 300 EDFSFDVLKLYEGGIKLPOGPLLKAITDSIPLEILKELLRSDGEGLFKYPTPQVIOEDK 359

Db 316 EDFSQDINELYEGGLKVANASALAEIKKRVPFELIKSLLPVAGDQVLKPLPHVikedK 375

QY 360 TAWRTDEEFGREMLAGVNPVIIISRLQEPFPKSKLDPKIYGNQNSTITREQIEDKLDGLTI 419

Db 376 FAWRTDEEFAREMLAGVNPVMIKRLTNPPAKSTLDPNVYGDHTSKITEAHIKHNMEGLTV 435

QY 420 DEAIKTNRLFILNHHDIIMPYLRRINTSTDTKTYASRTLFLQDNGTLKPSAIELSLPHP 479

Db 436 QNALKGNRLFILDHHDHFMFPFLDKINKLDGNFIYASRTILLKDDGTLPKLAIELSLPHP 495

QY 480 DGDFGAVSKVYTPADQGVESGIWOLAKAYAAVNDSGVHQLISHWLNTAAIEPFVIATN 539

Db 496 DGQOHGAVSKVYTPANTGVESQIWOLAKAYASVNDSAWHQLISHWLNTHAVIEPFVIATN 555

QY 540 QLSALHPIYKLLHPPHFRETNMNINALARQILINGGGLLELTVFPAKYSMEMSAVVYKDWV 599

Db 556 QLSVVHPVHKLLSPHYRDTMNINALARQTLINADGIFEKTVFPGKYALEMSSVVYKNWK 615

QY 600 FPEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKS 659

Db 616 FTEQALPVDLVKRGVAVDPDTPSYNVRLLIKDYPYAVDGLVWAIERWVGEYLAIYYPN 675

QY 660 DDAVQKDTLQAWWKELREEGHGDKDEPPWPKMQTVQELIDSCITITIIWIASALHAAVNF 719

Db 676 DGVLRGDEELQAWWKKEVREVGHDGLKDQDWPKMDTVQELTRACTIIIIWIASALHAAVNF 735

QY 720 GOYPYAGYLPNRPRTLNRNFMPEPGSPYEELKTNPKD--VFLKTIPTQLQTLGSLIE 776

Db 736 GOYPYAGYLPNRPRTVSRPMPEPGTEEYAKLERGGDEADLVFIHTITSQFQTLGSLIE 795

QY 777 ILSRHSSDLYLGQRESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPV 836

Db 796 ILSKHSSDEVILGQDTPWTSDAKALDAFKRFGSRLVDIENRIKDMNGNSALKNRNGPV 855

QY 837 KVPYTLFPPTSEG-----GLTKGIPNSVSI 862

Db 856 KMPYMLLYPNTSDVTKEKGQGLTAMGIPNSISI 888

RESULT 15

US-10-424-599-220216

; Sequence 220216, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 220216

; LENGTH: 860

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(860)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_40885C.1.pap

US-10-424-599-220216

Query Match 61.5%; Score 2790; DB 15; Length 860;

Best Local Similarity 60.9%; Pred. No. 1.4e-218;

Matches 525; Conservative 129; Mismatches 178; Indels 30; Gaps 7;

QY 17 KKVKGTVVLMMKNVLDFTDINA-----SVLDGVLEFLGRRVSLELISSVNAD 63

Db 13 QVKGTVVLMRKNVLDINSITSVRGLIGTGINIIGSTIDGLTSFLGRSVCLQLISATKAD 72

QY 64 -PANGLOGKRSKAAYLENWLNTSTPIAAGESAFRVTFDWDDEEFGVPGAFIINKLHFSEF 122

Db 73 GNGGVVGKKT--YLEGIITSIPTLGAGQSAFTIHFEW-DADMGIPGAFLIKNYMQVEL 128

QY 123 FLKSLTLEDVNPNGKVFHVCNSWVYPANKYKSDRIFFANQAYLPSETPTDLRKYRENELV 182

Db 129 FLVSLTLEDIPNQSGMHFVCNSWVYNSKVYEKDRIFFASETYVPSETPGPLVTYREAELQ 188

QY 183 TURGDGTGKLEEDRWVDYAYVNDLGDGDPKQDLSRPVLGSGSEYPYPRRGRTGRKPTKT 242

Db 189 ALRNGGTGKRKEWDRVYDYVDYNDLGNPDSENGFARPVLGSLTHPHYPRRGRTGRKPTKK 248

QY 243 DPNSERIPLLMSLDIYVPRDERFGHIKLSDFLTFALKSIVQLLLPEFKALFD--STHNE 300

Db 249 DPNSEK-----PGEAYIPRDENFGHLKSSDFLTGYLKSILTRSFPLAKTVFDINFTPNE 302

QY 301 FDSFEDVLKLYEGGIKLPOGPLLKAITDSIPLEILKELLRSDGEGLFKYPTPQVIOEDKT 360

Db 303 FDSFEVRALCEGGIKLPTDILSKI----SPLPVLKEIFRTDGESVLKFSVPDLIKVSKS 358

QY 361 AWRTEDEEFGREMLAGVNPVIIISRLQEPFPKSKLDPKIYGNQNSTITREQIEDKLDGLTID 420

Db 359 AWMTEDEEFAREMIAGVNPVIRRLQEPFPQSKLDPVSYGDTQSKMTIDHLEINLEGLTVD 418

QY 421 EAIKTNRLFILNHHDIIMPYLRRINTSTDTKTYASRTLFLQDNGTLKPSAIELSLPHPD 480

Db 419 KAIKDQRLFILDHHDTFMPFLRRIDESKSKAYATRITLFLKDDGTLPKLAIELSLPHPG 478

QY 481 GDQFGAVSKVYTPADQGVESGIWOLAKAYAAVNDSGVHQLISHWLNTAAIEPFVIATNR 540

Db 479 QQQLGAYSKVILPANQGVESTIWLAKAHVIVNDSYHQLISHWLNTHAVIEPFVIATNR 538

QY 541 QLSALHPIYKLLHPPHFRETNMNINALARQILINGGGLLELTVFPAKYSMEMSAVVYKDWVF 600

Db 539 NLSILHPIYKLLFPHYRDTMNINALARQSLINADGFIKTFLGKYAVEISSSGYKNWVF 598

QY 601 PEQALPTDLIKRGVAVEDSSSPLGIRLLIQDYPYAVDGLKIWSAIKSWVTEYCNYYKSD 660

Db 599 LDQALPADLIKRGMAIEDSSCENGLRLVIEDYPYAVDGLIEWDAIKTWVQEVVSLYYATN 658

QY 661 DAVQKDTLQAWWKELREEGHGDKDEPPWPKMQTVQELIDSCITITIIWIASALHAAVNF 720

Db 659 DAIKDHQLQAWWKKEVVEKGHGDLDKDPWPKMQTLQELIQSCSTIIWIASALHAAVNF 718

QY 721 QYPYAGYLPNRPRTLNRNFMPEPGSPYEELKTNPKDVKFLKTIPTQLQTLGSLIEILSR 780

Db 719 QYPYGGFILNRPRTLNRRIPEEGTPEYDEMTKNPQKAYLRTITPKFQALVDLSVIEILSR 778

QY 781 HSSDLYLGQRESPEWTKDQEPLSAFARFGKKLSDIEDQIMQMNVDKWKNRSGPVKVPY 840

Db 779 HASDEVYLGQRDNPNWTSNPKAIEAFKFKGXXKLAEIETKISERNHDPNLRNRTGPAQLPY 838

QY 841 TLLFPTSEGGLTGKIPNSVSI 862

Db 839 TVLLPTSETGLTFRGIPNSISI 860



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 13, 2005, 22:52:34 ; Search time 1087 Seconds  
(without alignments)  
4694.404 Million cell updates/sec

Title: US-10-731-642A-1  
Perfect score: 4534  
Sequence: 1 MFLEKIVDAITGKODGKKV.....LFPTSEGLTGKIPNSVSI 862

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO spo01/US10731642/runat 10032005 102235 5450/app\_query.fasta\_1.1031  
-DB=N Geneseq 16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10731642 @CGN 1 1 547 @runat 10032005 102235 5450 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :				N_Geneseq_16Dec04:*			
Result No.	Score	Query Match	Length	DB ID	1: Geneseqn1980s:*		
					2: Geneseqn1990s:*		
					3: Geneseqn2000s:*		
					4: Geneseqn2001as:*		
					5: Geneseqn2001bs:*		
					6: Geneseqn2002as:*		
					7: Geneseqn2002bs:*		
					8: Geneseqn2003as:*		
					9: Geneseqn2003bs:*		
					10: Geneseqn2003cs:*		
					11: Geneseqn2003ds:*		
					12: Geneseqn2004as:*		
					13: Geneseqn2004bs:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
					* Query Match	
1	4534	100.0	3390	8	ABZ68210	Abz68210 Nucleotid
2	3620.5	79.9	2871	2	AAT60428	Aat60428 Tomato fr
3	3463.5	76.4	2441	2	AAT60429	Aat60429 Tomato fr
4	3254.5	71.8	4237	9	ACD28852	Acd28852 Wine grap
5	3202.5	70.6	2580	6	ABZ13699	Abz13699 Arabidops

6	3202.5	70.6	2580	8	ADA67958	Ada67958 Arabidops
7	3138	69.2	4687	9	ACD28851	Acd28851 Wine grap
8	3054	67.4	2562	8	ABX13452	Abx13452 A. thalia
9	3022.5	66.7	2929	9	AA157712	Aal57712 Balsam pe
10	2911	64.2	2964	4	AAF88022	Aaf88022 Cucumber
11	2911	64.2	2964	8	ABX13453	Abx13453 C. sativu
12	2779.5	61.3	2595	10	AA64729	Aad64729 Maize lip
13	2779.5	61.3	3007	10	AA64728	Aad64728 Maize lip
14	2769.5	61.1	2595	10	ADG93380	Adg93380 Maize lip
15	2769.5	61.1	3007	10	ADG93378	Adg93378 Maize lip
16	2734.5	60.3	2664	10	ADG93388	Adg93388 Maize lip
17	2734.5	60.3	3080	10	ADG93386	Adg93386 Maize lip
18	2724.5	60.1	2664	10	ADG93396	Adg93396 Maize lip
19	2724.5	60.1	2664	10	ADG93392	Adg93392 Maize lip
20	2724.5	60.1	3122	10	ADG93390	Adg93390 Maize lip
21	2724.5	60.1	3134	9	AA157714	Aal57714 Corn (Zea
22	2700.5	59.6	2622	10	ADG93372	Adg93372 Maize lip
23	2700.5	59.6	2912	10	ADG93370	Adg93370 Maize lip
24	2694.5	59.4	2613	8	ADA69728	Ada69728 Rice gene
25	2682	59.2	3033	10	ADC53127	Adc53127 9'-specif
26	2680	59.1	2818	6	ABK88441	Abk88441 Barley li
27	2680	59.1	2818	6	ABK88515	Abk88515 DNA encod
28	2654.5	58.5	2559	8	ADA70433	Ada70433 Rice gene
29	2605	57.5	2516	9	ADA48505	Ada48505 Rice gene
30	2585.5	57.0	2616	10	ADG93384	Adg93384 Maize lip
31	2585.5	57.0	2949	10	ADG93382	Adg93382 Maize lip
32	2563	56.5	2830	2	AAQ24492	Aaq24492 Rice lipo
33	2563	56.5	2830	2	AAQ24234	Aaq24234 Lipoxigen
34	2404.5	53.0	2566	12	ADJ39813	Adj39813 Plant cDN
35	2386	52.6	2115	8	ADA69794	Ada69794 Rice gene
36	2329.5	51.4	7059	2	AAQ44750	Aaq44750 Soybean l
37	2280.5	50.3	4663	6	ABK88440	Abk88440 Barley li
38	2280.5	50.3	4663	6	ABK88514	Abk88514 Wild type
39	2280.5	50.3	4663	6	ABK88522	Abk88522 DNA encod
40	2273.5	50.1	4663	6	ABK88445	Abk88445 Barley li
41	2273.5	50.1	4663	6	ABK88442	Abk88442 Barley li
42	2273.5	50.1	4663	6	ABK88521	Abk88521 DNA encod
43	2273.5	50.1	4663	6	ABK88516	Abk88516 DNA encod
44	2259	49.8	4483	10	ADG93425	Adg93425 Maize lip
45	2259	49.8	7492	10	ADG93422	Adg93422 Maize lip

ALIGNMENTS

RESULT 1	
ABZ68210	
ID	ABZ68210 standard; DNA; 3390 BP.
XX	
AC	ABZ68210;
XX	
DT	07-APR-2003 (first entry)
XX	
DE	Nucleotide sequence comprising CaMV 35S promoter and tobacco LOX1.
XX	
KW	Lipoxygenase-1; LOX-1; enzyme; plant; dioxygenation;
KW	polyunsaturated fatty acid; pentadiene; disease resistance; Solanacea;
KW	tobacco; tomato; potato; pepper; gene; ss.
XX	
OS	Nicotiana tabacum.
XX	
FH	Key
FT	promoter
FT	1..532
FT	/*tag= a
FT	/note= "CaMV 35S promoter"
FT	543..3131
FT	/*tag= b
FT	/product= "LOX1"
FT	/note= "6"
FT	3138..3390
FT	terminator
FT	/*tag= c
FT	/note= "Nos terminator"
XX	
PN	WO200299112-A2.

XX 12-DEC-2002.  
PD 06-JUN-2002; 2002WO-FR001943.  
XX 07-JUN-2001; 2001FR-00007470.  
PR 07-NOV-2001; 2001FR-00014358.  
XX (RHOB-) RHOBIO.  
PA  
XX Mene-Safrane L, Esquerre-Tugaye M, Fournier J, Beffa R;  
PI Grosjean-Cournoyer M;  
PI  
XX  
DR WPI; 2003-156858/15.  
DR P-PSDB; ABP70404.  
XX  
PT Reducing sensitivity of plants to diseases and pathogens, by  
PT overexpressing a lipoxigenase, also vectors and cassettes for the process  
PT and transformed plants.  
XX  
PS Example 2; Page 42-46; 47pp; French.  
XX  
CC The present sequence encodes a lipoxigenase-1 (LOX-1) gene. LOX-1 is an  
CC enzyme that catalyses the dioxygenation of polyunsaturated fatty acids  
CC having a pentadiene system. Overexpression of LOX-1 can be used to reduce  
CC the sensitivity of plants to diseases and attack by pathogens.  
CC Overexpression of LOX-1 improves resistance to viruses, bacteria, fungi  
CC and insects, in a wide range of crops, particularly the Solanaceae, e.g.  
CC tobacco, tomato, potato and pepper  
XX  
SQ Sequence 3390 BP; 1067 A; 698 C; 742 G; 883 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 0 Length: 3390  
Score: 4534.00 Matches: 862  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0  
  
US-10-731-642A-1 (1-862) x ABZ68210 (1-3390)  
  
Qy 1 MetPheLeuGluLysIleValAspAlaIleThrGlyLysAspAspGlyLysLysValLys 20  
Db 543 ATGTTCTGGAGAAGATTGTGGATGCAATCACAGGGAAGATGATGGAAAAAGGTAAAA 602  
  
Qy 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40  
Db 603 GGAACAGTGGTTTTTGATGAAGAAAAAATGTTTGGATTTTACTGATATTAAATGCCTCAGTT 662  
  
Qy 41 LeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerVal 60  
Db 663 CTTGATGGAGTCTTTGAGTTCCTTGGTCGGAGGGTCTCTCTCGAGTTGATCAGTTCTGTT 722  
  
Qy 61 AsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsn 80  
Db 723 AATGCTGATCCTGCAAAATGGTTTACAAGGGAAACGCAGCAAAGCAGCATATTGGAGAAC 782  
  
Qy 81 TrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAsp 100  
Db 783 TGGCTAACAAATAGCACCCCAATAGCAGCAGGTGAATCAGCATTTAGAGTCACATTTGAT 842  
  
Qy 101 TrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSer 120  
Db 843 TGGGATGATGAGGAATTTGGAGTTCAGGAGCATTCATTATCAAGAACTTGGCATTTTGT 902  
  
Qy 121 GluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPhe 140  
Db 903 GAGTCTTCTCCTCAAGTCACTACCTTGAAGATGTTTCCATAATCATGGCAAGTTTCATTT 962  
  
Qy 141 ValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAla 160  
Db 963 GTCTGTAATTCTTGGGTTTATCCTGCTAAATAAATAATAAGTCAGATCGCATCTTCTTCGG 1022

Qy 161 AsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGlu 180  
Db 1023 AATCAGGCTTATCTACCAAGTGAACACCAGACACATTGGCAAAATACAGAGAAATGAA 1082  
  
Qy 181 LeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArgValTyrAsp 200  
Db 1083 TTAGTAACCTTAAGAGGAGATGGAACCTGGAAGCTTGAGGAATGGGATAGAGTTTATGAC 1142  
  
Qy 201 TyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProVal 220  
Db 1143 TATGCTTACTACAATGACTTGGGTGATCCAGACAAGGCCAAGATTGTCAAGGCCTGTC 1202  
  
Qy 221 LeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThr 240  
Db 1203 TTAGGAGGATCTTCTGAGTACCCGTATCCTCGTAGAGGAGGACAGGCCGCAACCAACC 1262  
  
Qy 241 LysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrVal 260  
Db 1263 AAAACAGATCCTAATCCGAGAGCAGGATTCCATTGCTTATGAGCTTAGACATATATGTG 1322  
  
Qy 261 ProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLys 280  
Db 1323 CCAAGGGACGAGCGATTGTTGTCATATAAAGTTGTGAGACTTCTTGACATTTGCTTTGAAA 1382  
  
Qy 281 SerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGlu 300  
Db 1383 TCCATTGTGCAGTTGCTTCTCCCTGAGTTTAAAGGCTTTGTTGATAGCAGCATAATGAG 1442  
  
Qy 301 PheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeuProGlnGly 320  
Db 1443 TTTGATAGTTTGGAGGATGTTAACTGATGAAGGAGGAATCAAGTTGCCTCAAGGC 1502  
  
Qy 321 ProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuArg 340  
Db 1503 CCTTTGTTGAAAGCCATTACTGATAGCATTCCTTTAGAGATACTAAAGAACTCCTTCGA 1562  
  
Qy 341 SerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAspLysThr 360  
Db 1563 AGTGATGGTGAAGGCCTATTAAAGTACCCAACTCCTCAGGTTATTCAAGAGGATAAAACT 1622  
  
Qy 361 AlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIle 380.  
Db 1623 GCATGGAGGACGGATGAAGAAATTTGGGAGAGAAATGTTGGCGGAGTCAATCCTGTGATA 1682  
  
Qy 381 IleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsn 400  
Db 1683 ATCAGTAGACTCCAAGAAATTCCTCCGAAAAGCAAGTTGGATCCTAAAATATATATGGCAAC 1742  
  
Qy 401 GlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAsp 420  
Db 1743 CAAAACAGTACAATTACCAGAGAGCAGATAGAGGATAAGTTGGATGGACTAACAATTGAT 1802  
  
Qy 421 GluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyr 440  
Db 1803 GAGGCAATCAAGACTAACAGACTATTTCATATTGAACCATCATGATATCCTTATGCCATAC 1862  
  
Qy 441 LeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPhe 460  
Db 1863 TTGAGGAGAAATTAACACGTCGACAGACACAAAAACCTATGCTCAAGAACTCTGCTCTTC 1922  
  
Qy 461 LeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAsp 480  
Db 1923 TTGCAAGATAATGGAACCTTTGAAGCCCATCAGCAATTGAACCTTAAGCTTGCCACATCCAGAC 1982  
  
Qy 481 GlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGly 500  
Db 1983 GGAGATCAATTTGGCGCTGTAGCAAAAGTATATACACCAGCTGATCAAGGTGTTGAAGGT 2042  
  
Qy 501 SerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeu 520  
Db 2043 TCTATCTGGCAGTTGGCCAAAGCCTATGCAGCAGTGAATGATTCGGGCGTTTCATCAACTC 2102

QY 521 IleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArg 540  
Db 2103 ATCAGTCACTGGTTGAATACACATGCAGCGATAGAGCCATTCTGTGATCGCAACAAATAGG 2162  
QY 541 GlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMet 560  
Db 2163 CAACCTAAGCGCGCTCACCCCTATTATATAAGCTCTCCACCCCTCAATTCCTCGTGAGACGATG 2222  
QY 561 AsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThr 580  
Db 2223 AACATAAATGCTTAGCAAGACAGATCTTGATCAACGGTGGTGGACTTCTTGAGTTGACA 2282  
QY 581 ValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhe 600  
Db 2283 GTTTTTCCGGCCAAATATTCCATGGAAATGTCAGCAGTAGTTTACAAAGACTGGGTTTTTC 2342  
QY 601 ProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSer 620  
Db 2343 CCTGAACAAGCACTTCCTACTGATCTCATCAAAGAGGAGTAGCTGTTGAGGACTCGAGC 2402  
QY 621 SerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLys 640  
Db 2403 TCCCCACTTGGCATTGATTTACTGATTCAGGACTATCCATATGCTGTGATGGTTGAAA 2462  
QY 641 ileTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrLysSerAsp 660  
Db 2463 ATTTGGTCAGCAATTAAAGTTGGTAACTGAATACTGCAACTACTATTACAAATCAGAT 2522  
QY 661 AspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGly 680  
Db 2523 GATGCGGTTCAAAAAGACACTGAACTCCAAAGCTGGTGAAGGAACTCCGGAAGAGGGA 2582  
QY 681 HisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIle 700  
Db 2583 CACGGTGACAAAGAAAGATGAGCCTTGGTGGCTTAAATGCAGACAGTGAAGAATTGATA 2642  
QY 701 AspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaValAsnPheGly 720  
Db 2643 GACTCTTGACCATCACAAATATGGATAGCTTCAGCACTTCATGTCAGCAGTCAATTTTCGGG 2702  
QY 721 GlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetPro 740  
Db 2703 CAATACCCCTATGCTGGTTATCTCCCTAATCGCCCTACATTAAAGCCAAATTCATGCCA 2762  
QY 741 GluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeuLys 760  
Db 2763 GAGCCAGGAGTCTCTGAGTATGAAGAGCTCAAGACAAATCCGGATAAGGTATTCTCTCAA 2822  
QY 761 ThrIleThrProGlnLeuGlnThrLeuGlyIleSerLeuIleGluIleLeuSerArg 780  
Db 2823 ACAATCACTCTCAGCTGCAGACACTGCTGGCATTTCCCTCATAGAGATCTTGTCAAGG 2882  
QY 781 HisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGln 800  
Db 2883 CATTCCTCGGATACACTTTACCTCGGCAAGGAATCACCTGAATGGACAAAGGATCAA 2942  
QY 801 GluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIle 820  
Db 2943 GAACCACTTTCAGCTTTTTCGAGGTTTGGAAAGAGCTGAGTGATATCGAGGATCAGATT 3002  
QY 821 MetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyr 840  
Db 3003 ATGCAGATGAATGTCGATGAGAAATGGAAGACAGGTCTGGTCCCTGTTAAAGTTCCATAC 3062  
QY 841 ThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerVal 860  
Db 3063 ACCTTGCTCTTCCCCACAAGTGAAGGAGGACTTACTGGCAAGGAATTCCTAACAGTGTG 3122  
QY 861 SerIle 862  
Db 3123 TCAATA 3128

AAT60428  
ID AAT60428 standard; cDNA; 2871 BP.  
XX  
AC AAT60428;  
XX  
DT 27-AUG-2003 (revised)  
DT 08-JUL-1997 (first entry)  
XX  
DE Tomato fruit ripening specific lipoxygenase gene.  
XX  
KW LOX gene; fruit ripening specific lipoxygenase; FRS-LOX; tomato;  
transgenic plant; ss.  
XX  
OS Lycopersicon esculentum.  
XX  
FH Key Location/Qualifiers  
FT primer\_bind 281..297  
FT /\*tag= a  
FT /note= "primer used to amplify a FRS-LOX gene fragment  
(nucleotides 1-297)"  
FT  
XX WO9713851-A1.  
PN  
XX 17-APR-1997.  
PD  
XX  
PF 11-OCT-1996; 96WO-US016387.  
XX  
PR 13-OCT-1995; 95US-0005404P.  
XX  
PA (PURD ) PURDUE RES FOUND.  
XX  
PI Handa AK, Kausch KD;  
XX  
DR WPI; 1997-235887/21.  
XX  
PT New transgenic plants with fruits having improved quality - obtained by  
transforming plant cells so as to inhibit production of fruit ripening  
specific lipoxygenase in fruits.  
XX  
PS Claim 5; Fig 4; 38pp; English.  
XX  
CC A tomato fruit ripening specific lipoxygenase (FRS-LOX) gene cDNA clone  
(AAT60428) was isolated from a red-ripe pericarp library using antibodies  
raised against a 90 kDa protein that accumulates in ripe fruit. The cDNA,  
or fragments of it (see also AAT60429-30), can be incorporated, in sense  
or antisense orientation, into vectors under control of e.g. the CaMV 35S  
promoter. The vectors are used to create transgenic fruit-bearing plants,  
esp. tomato, in which native FRS-LOX gene expression is inhibited. These  
plants can provide fruits having superior characteristics such as  
improved quality and texture, greater firmness, longer shelf life, better  
packaging and storage characteristics and improved processing  
characteristics. (Updated on 27-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 2871 BP; 888 A; 545 C; 614 G; 824 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 0 Length: 2871  
Score: 3620.50 Matches: 684  
Percent Similarity: 87.37% Conservative: 70  
Best Local Similarity: 79.26% Mismatches: 104  
Query Match: 79.85% Indels: 5  
DB: 2 Gaps: 3  
  
US-10-731-642A-1 (1-862) x AAT60428 (1-2871)  
  
QY 1 MetPheLeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysLysValLys 20  
Db 45 ATGTCCTTGGTGGAAATTGTGGATGCCATCTTGGAAAAGATAGAGCCAAAGTGAAA 104  
QY 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40  
Db 105 GGAAGAGTGATTTTGTGATGAAAAAAAATGTTCTAGACTTCATTATATAGGTGCTTCAGTT 164





Db	2313	AAAA	CATTTG	TTCCTC	AGTTG	CAATCA	CTGCTT	GAAATTT	CCATCTT	TGAGG	CTCGTCA	2377
QY	780	ArgHis	SerSer	AspThr	LeuTyr	LeuGly	GlnArg	GluSer	ProGlu	TrpThr	LysAsp	799
Db	2373	AGGC	ATGCTT	CAGATG	AGGTTT	ACTTTG	GGACAA	AGGGA	CTCA	ATTGA	TGGACAA	2432
QY	800	GlnGlu	ProLeu	SerAla	PheAla	ArgPhe	GlyLys	LysLeu	SerAsp	IleGlu	AspGln	819
Db	2433	AAAG	AACCA	CTTGT	AGCTTT	GAGAGG	TTTGG	AAGATG	CTTAA	GTGAT	ATCGAGA	2492
QY	820	IleMet	GlnMet	AsnVal	AspGlu	Lystrp	LysAsn	ArgSer	GlyPro	ValLys	Valpro	839
Db	2493	ATTAT	GATAAT	GAATAG	TATCATA	AAGAGT	TGGAAG	AACAGG	TCAAGG	CCCTGT	TAACTTCCA	2552
QY	840	TyrThr	LeuLeu	PhePro	ThrSer	GluGly	GlyLeu	ThrGly	LysGly	IlePro	AsnSer	859
Db	2553	TATAC	GTGCT	CTCTTT	CCCA	CAAGTGA	AGAGG	GACTC	ACAGG	CAAA	AGGAATTTCC	2612
QY	860	ValSer	Ile	862								
Db	2613	GTGT	CTATA	2621								

RESULT 3  
AAT60429

ID AAT60429 standard; cDNA: 2441 BP.

AC AAT60429;

DT 27-AUG-2003 (revised)

DT 08-JUL-1997 (first entry)

Tomato fruit ripening specific lipoxygenase gene fragment.

LOX gene; fruit ripening specific lipoxygenase; FRS-LOX; tomato; transgenic plant; ss.

OS *Lycopersicon esculentum*.

PN WO9713851-A1.

PD 17-APR-1997.

PF 11-OCT-1996; 96WO-US016387.

PR 13-OCT-1995; 95US-0005404P.

PA (PURD ) PURDUE RES FOUND:

PI Handa AK, Kausch KD;

DR WPI; 1997-235887/21.

New transgenic plants with fruits having improved quality - obtained by transforming plant cells so as to inhibit production of fruit ripening specific lipoxigenase in fruits.

PS Claim 6; Fig 1; 38pp; English.

A tomato fruit ripening specific lipoxigenase (FRS-LOX) gene fragment (AAT60429) comprises nucleotides 158-2598 of the FRS-LOX gene (see also AAT60428). It was isolated from partial LOX cDNA clone 8-27-1, and can be inserted into the multiple cloning site present between the CamV 35S promoter and rbc 3' terminator sequences in pTZ35rbss in both orientations, yielding pTZSL (sense) and pTZAL (antisense). These vectors can be used to create transgenic fruit-bearing plants, esp. tomato, in which native FRS-LOX gene expression is inhibited. These transgenic plants can provide fruits having improved quality and texture, greater firmness, longer shelf life, better packaging and storage characteristics and improved processing characteristics. (Updated on 27-AUG-2003 to correct OS field.)

Sequence 2441 BP; 742 A; 496 C; 544 G; 659 T; 0 U; 0 Other;

Alignment Scores:		0	Length:	2441
Pred. No.:	Score:	3463.50	Matches:	650
Percent Similarity:		87.88%	Conservative:	68
Best Local Similarity:		79.56%	Mismatches:	94
Query Match:		76.39%	Indels:	5
DB:		2	Gaps:	3
US-10-731-642A-1 (1-862) x AAT60429 (1-2441)				
QY	39	SerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSer	58	
DB	2	TCAGTTGTTGATGGCAATTTCTGATTTACTTGGCCAAAAGTCTCTATCCAATTGATAAGT	61	
QY	59	---SerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyr	77	
DB	62	GGTTCTGTTAATTATGAT-----GGTTTGGAAAGGAAACTGAGCAATCCAGCATAC	112	
QY	78	LeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgVal	97	
DB	113	TTAGAGAGTTGGCTTACAGACATCACCCCAATAACAGCAGGGGAATCAACTTTTAGTGTT	172	
QY	98	ThrPheAspTrpAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeu	117	
DB	173	ACATTTGACTGGGATCGTGACGAGTTTGGAGTTCCAGGAGCATTCATCATCAAGAATCTT	232	
QY	118	HisPheSerGluPheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLys	137	
DB	233	CATCTTAATGAGTCTTTCTCAAGTCACCTCACACTCGAAGATGTTCTTAATTATGGAAA	292	
QY	138	ValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIle	157	
DB	293	ATCCATTTTGATGCAATCTTGGGTTTATCCTGCTTTTAGATACAAGTCTGACCGCATT	352	
QY	158	PhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArg	177	
DB	353	TTCTTTGCCAATCAGGCTTATCTCCAAAGTGAACACACCACCAATTCGAAAAATACAGA	412	
QY	178	GluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArg	197	
DB	413	GAAAATGAACCTGGTAGCTTTCGAGGAGATGGAACTGGAAAGCTTGAAGAATGGGACAGG	472	
QY	198	ValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSer	217	
DB	473	GTTTATGATTATGCTTCCTACAAATGACTTGGGTGAACCCAGATAAGGGGAAGAGTATGCT	532	
QY	218	ArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArg	237	
DB	533	AGGCCTATCCCTGGAGGTCTCTGAGTACCCGTATCCCTCGTAGAGGCAGGACAGGCCGC	592	
QY	238	LysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAsp	257	
DB	593	GAACCAACCAAGCAGATCCTAATTGCGAGAGCAGGAACCCATTCCTATGAGCTTAGAC	652	
QY	258	IleTyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPhe	277	
DB	653	ATATATGTCCCAAGGACGAGCGATTTGGTCATGTGAAGAAGTCTGAGCTTTTGACGTCG	712	
QY	278	AlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThr	297	
DB	713	TCCTTAAAAATCCTTTTGCAACCGCTTCTCCCTGCGTTTAAAGGCTTTGTGCGATAACACG	772	
QY	298	HisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeu	317	
DB	773	CCTAATGAGTTCAATAGCTTTGCGGATGTACTTAATCTCTATGAAGGAGGAATCAAGTTG	832	
QY	318	ProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGlu	337	
DB	833	CCTGAAGGCCCTTGGTTGAAAGCCATTACTGTATAACATTTCTCTCAGAGATACTAAAGAC	892	
QY	338	LeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGlu	357	
DB	893	ATCCTTCAAACGGATGTTCAAGGCCCTACTTAAGTACCCAACTCTCTCAGGTTATTCAAGGC	952	

QY	358	AspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsn	377
DB	953	GATAAACTGCATGGAGCGGATGAAGAAATTTGGGAGAGAAATGTTGGCAGGATCCAAT	1012
QY	378	ProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIle	397
DB	1013	CCTGTCTTAATCAGTAGACTCCAAGAATTTCTCCGAAGAGCAAGTTGGATCCAACCATTA	1072
QY	398	TyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeu	417
DB	1073	TATGGAAACCAAAACAGTACAATTACCACAGAACATGTACAGGATAAGTTGAATGGATTA	1132
QY	418	ThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeu	437
DB	1133	ACAGTGAATGAGGCAATCAAGAGTAACAGGTTATTTCATATTGAACCAACCATGACATCGTG	1192
QY	438	MetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThr	457
DB	1193	ATGCCACTATTGAGGAAATTAACATGTACAGCAACACAAAAGCCTATGCCTCAAGAACT	1252
QY	458	LeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuPro	477
DB	1253	CTGCTCTTCTACAGATGATAGAACTTTGAAGCCACTAGCAATTGAACCTAAGCTTGCCA	1312
QY	478	HisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGly	497
DB	1313	CATCCAGACGGAGATCAATTTGGTACTGTTAGTAAAGTATATACACCAGCTGACCAAGGT	1372
QY	498	ValGluGlySerIleTrpGlnLeuAlaLysAlaValSerLysValTyrThrProAlaAspGlnGly	517
DB	1373	GTTGAAGGTTCTATCTGGCAGTTTGCCAAAGCCTATGTAGCAGTGAATGACATGGGCATT	1432
QY	518	HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAla	537
DB	1433	CATCAGCTCATTAGCCACTGGTTGAATACACACGGGTGATCGAACCATTTGTGATTGCA	1492
QY	538	ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg	557
DB	1493	ACAAATAGGCATCTAAAGTGTGCTTCCATCCCATTTCATAAACTTCTTCATCCTCATTTCCGT	1552
QY	558	GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeu	577
DB	1553	AACACGATGAACATAAATGCTTTAGCAAGAGAGACCTTGACCTATGATGGTGGT--TTT	1609
QY	578	GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp	597
DB	1610	GAGACGTCTCTTTTCTCTGCCAAATATTCCATGGAATGTGAGCAGCAGCTTACAAGAT	1669
QY	598	TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGlu	617
DB	1670	TGGGTTTTCCCTGAACAAGCATTCTCTGCTGATCTCTCAAAGAGGAGTGGCTGTGAG	1729
QY	618	AspSerSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAsp	637
DB	1730	GACTTGAGCTCCCCACATGGCATTCGTTTACTGATTCTGGACTATCCATATGCTGTTGAT	1789
QY	638	GlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyr	657
DB	1790	GGCTTGGAAATTTGGGCAGCAATCAAAAGTTGGGTAACAGAAATATTGCAAGTTCTATTAC	1849
QY	658	LysSerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArg	677
DB	1850	AAATCTGACGACACGTAGAGAAAGACACTGAACCTCAAGCTTGGTGAAGGAGCTCCGC	1909
QY	678	GluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGln	697
DB	1910	GAAGAAGGACATGGCGACAAGAAAGATGAGGCTTGGTGGCCTAAACTGCAAACTCGACA	1969
QY	698	GluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaVal	717
DB	1970	GAGCTCAGAGATTGTTGCACCATCATTTATATGGATAGCTTCAGCACTTTCATGCGACTC	2029

QY	718	AsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsn	737
DB	2030	CATTTTGGCTTATACTCTTACGCTGGTTATCTCCCTAATCGCCCTACTTTAAGCTGTAAT	2089
QY	738	PheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysVal	757
DB	2090	TTGATGCCAGAGCCAGGAAGTGTGTAGTATGAAGAGCTCAAGACAAATCCAGACAAGGTA	2149
QY	758	PheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIle	777
DB	2150	TTCTCTAAAAACATTTGTTCTCCTCAGTTGCAATCACTGCTTGAAATTTCCATCTTTGAGGTC	2209
QY	778	LeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyrThr	797
DB	2210	TCGTCAAGGCATGCTTCAGATGAGGTTTACTTGGGACAAAGGGACTCAATTGAATGGACA	2269
QY	798	LysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGlu	817
DB	2270	AAGGATAAAGAACCACTTGTAGCTTTTGAGAGGTTTGGAAAGATGCTAAGTGATATCGAG	2329
QY	818	AspGlnIleMetGlnMetAsnValAspGluLysTyrLysAsnArgSerGlyProValLys	837
DB	2330	AATCGAATTATGATAATGAATAGTCATAAGAGTTGGAAGAACAGGTGAGGCCTGTTAAC	2389
QY	838	ValProTyrThrLeuLeuPheProThrSerGluGlyLeuThrGlyLys	854
DB	2390	GTTCCATATACGTTGCTCTTTCCCAAGTGAAGAGGGACTCACAGGCAAA	2440
RESULT 4			
ACD	28852		
ID	ACD28852	standard; DNA; 4237 BP.	
XX	ACD28852;		
XX	27-AUG-2003	(first entry)	
DT			
XX	Wine grape lipoxxygenase LOX2 DNA.		
KW		Wine grape; ds; lipoxxygenase; LOX; flavour; fermented beverage; wine;	
KW		grape juice; cheese; yogurt; pickle; tissue specificity; timing; gene.	
OS		Vitis vinifera.	
XX			
PN	US2003033627-A1.		
PD	13-FEB-2003.		
XX			
PF	16-OCT-2001; 2001US-00978522.		
XX			
PR	16-OCT-2000; 2000US-0241220P.		
XX			
PA	(DESC/) DESCENZO R A.		
PA	(IREL/) IRELAN N A.		
XX			
PI	Descenzo RA, Irelan NA;		
XX			
DR	WPI; 2003-492095/46.		
DR	P-PSDB; ABO19443.		
XX			
PT	Novel purified and isolated Vitis vinifera lipoxxygenase polypeptide,		
PT	useful for modifying the flavor of a comestible e.g., a beverage which is		
PT	a fermentation product, preferably wine.		
XX			
PS	Claim 1; Page 16-17; 36pp; English.		
XX			
CC	The invention relates to a purified and isolated Vitis vinifera		
CC	lipoxxygenase (LOX) polypeptide. The polypeptide is useful for modifying		
CC	the flavour of a comestible e.g. a beverage which is a fermentation		
CC	product, preferably wine. The polypeptide is useful for analysing the		
CC	effect of LOX polypeptides on flavour production in wine and grape juice.		
CC	The polypeptide is useful in the production of cheese, yogurt, pickles		
CC	etc. The polypeptide is also useful in screening assays to identify		
CC	modulators that modulate the activity of the Vitis vinifera LOX		





Qy 383 ----- 383  
Db 1740 TACAGCTTCCTTTCAAAATATTTTAAATGCCCTGTTTGTGTTTCTGAGAAAATGGAACITG 1799  
Qy 383 ----- 383  
Db 1800 GAAAGGCTTCCAGACTTTGTGTTTCTTCCCTCCATCTACTGTGTTCTAGCTCTTTTCTGTATA 1859  
Qy 384 -----LeuGlnGluPheProProLysSerLysLeuAspProL 396  
Db 1860 ATTATTGGCTTTTCTACTTTGTTTGCAGGAGTTTCCCTCCAAAAGCAAGCTGGATCCTG 1919  
Qy 396 ysileTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspG 416  
Db 1920 AAGTTATGGCAACCAAAACAGTTCAATAACCAAGAACAACATAGAGAATCACCTGGATG 1979  
Qy 416 lyLeuThrIleAspGluAla----- 422  
Db 1980 ACCTTACTATAAACGAGGT-AACGCTCTTAGGTTCCCTTCTTTCAGACTAAATTTTTCAA 2038  
Qy 422 ----- 422  
Db 2039 TGTCGACATGTTAATTTTTTGCAATTGGAACACAAGCCATAGTAAGTGAATAATGGTGCTT 2098  
Qy 423 -----IleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetP 439  
Db 2099 TTTTACTAGGCAATGGAGAAGAGGCTATTTCATATTAGATCACCATGATGTTTTCATGC 2158  
Qy 439 roTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuL 459  
Db 2159 CATACCTGAGGAGGATAAACACA---ACTTCCAGGAAACCTTATGCTCAAGGACTCTCC 2215  
Qy 459 eupheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisP 479  
Db 2216 TCCTTCTGAAAGACGACGGAACCTTTGAAGCCACTGGCGATTGAATTGAGCTTACCACATC 2275  
Qy 479 roAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValG 499  
Db 2276 CTAGTGGGATAAAATTGGAGCTGTCAACAAAGTATATACGCCAGCTGAAAATGGTGTTG 2335  
Qy 499 luGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisG 519  
Db 2336 AAGGTTCCATTGGCAGCTGGCTAAAGCTTATGCTGCTGTGAATGACTCTGGCTATCATC 2395  
Qy 519 lnLeuIleSerHisTrpLeu----- 525  
Db 2396 AGCTCCTCAGCCACTGGTA-TGTAATATCCCAAGGAAAGTGAATACAGTTTGGGCTTAA 2454  
Qy 526 -----AsnThrHisAlaAlaI 531  
Db 2455 ATCTGAAGCGGTTGTGAATATCTTTGATGTTGGTTGCAGTTGAATACACATGCTGCAA 2514  
Qy 531 leGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysL 551  
Db 2515 TTGAGCCATTGTGATTGCAACCAACAGGCAGCTCAGCGTGCTTCATCCAATTCAACAAGC 2574  
Qy 551 euLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuI 571  
Db 2575 TTTTGGCATCCTCACTTCCGTGATACAATGAATATAAATGCATTAGCTCGACAAATCCTCA 2634  
Qy 571 leAsnGlyGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMetS 591  
Db 2635 TCAATGCTGGTGGAGTGGTGAGACACAGTTTTTCCATCAAAAGTATGCCATGGAAATGT 2694  
Qy 591 erAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleL 611  
Db 2695 CATCTGTGTTTACAAGACTGGGTCTTACTAGCAAGCACTTCTGCTGTATCTCATCA 2754  
Qy 611 ys----- 611  
Db 2755 A-GAGGTATATAAAATACTGTTAGTGATGTTTCTTCTCCTGCTGTGGAATGAATCTAGTG 2813  
Qy 612 -----ArgGlyVala 615

Db 2814 AAAATTGTGATTTTCACTAACTGATATGCTGCAACTTGGGCACCTCTTTTCAGAGGAATGG 2873  
Qy 615 laValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrA 635  
Db 2874 CGGTTGAGGATTCAGAGGCTCCTCATGGACTCCGCCTACTGATAGATGACTACCCCTATG 2933  
Qy 635 laValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnT 655  
Db 2934 CTGTTGATGGACTTGAGATCTGGTCAGCTATTGAGACATGGTGAAAAGAGTATTGCTCAT 2993  
Qy 655 yrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTyrLysG 675  
Db 2994 TCTACTACAAGACAGATGAGATGGTCCAGAAAGACTCTGAGCTTCAGTCTCTGGTGAAGG 3053  
Qy 675 luLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnT 695  
Db 3054 AAGTCAGGGAAGAGGGTCAATGGCGACAAGAAGGACGAGCCCTGGTGGCCTAAATGCATA 3113  
Qy 695 hrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisA 715  
Db 3114 CTGTCAAAGAGCTGATAGAAACATGCACCATTATCATCTGGGTGGCTTCTGCTCTCCATG 3173  
Qy 715 laAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuS 735  
Db 3174 CTGCAGTGAATTTCCGGGCACTACCTTATGCAGGCTACCTCCAAAACCGCCCAACGATAA 3233  
Qy 735 erArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProA 755  
Db 3234 GCCGAGATTCATGCCTGAAGAAGGCACCTCCTGAGTATGAAGAACTCAAGTCCAATCCTG 3293  
Qy 755 spLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuI 775  
Db 3294 ATAAGGCTTTCCTGAAAACAATCACTGCCAGCTGCAGACCCCTTCTTGGCATCTCCCTTA 3353  
Qy 775 leGluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProG 795  
Db 3354 TTGAGGTCCTTTCCAGGCATTTCTTCCGATGAGGTTTATCTTGGACAGAGACACTCCTG 3413  
Qy 795 luTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerA 815  
Db 3414 AATGGACCTGGACACAACACCATTTGAAAGCTTTTGAGAAATTCGGAAGGAAGCTGGCAG 3473  
Qy 815 spIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyP 835  
Db 3474 ACATTGAAGAAATGATCATAGATAGAAAATGGAATGAGAGATTCAAGAAACAGAGTTGGGC 3533  
Qy 835 roValLysValProTyrThrLeuLeuPheProThrSerGluGlyLeuThrGlyLysG 855  
Db 3534 CTGTGAAGATACCATACACTGCTCTACCCCAAGCGAAGGTGGGCTTACTGGCAAAG 3593  
Qy 855 lyIleProAsnSerValSerIle 862  
Db 3594 GGATTCCCAACAGTGTCTCCATC 3616  
RESULT 5  
ABZ13699  
ID ABZ13699 standard; DNA; 2580 BP.  
XX AC ABZ13699;  
XX 21-JAN-2003 (first entry)  
DT XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1504.  
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX Arabidopsis thaliana.  
XX WO200216655-A2.  
PN XX  
XX 28-FEB-2002.  
PD XX





Qy 518 HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAla 537  
|||||  
Db 1540 CATCAGCTTATTAGCCACTGGATGCAAAACACACGCATCGATTGAACCGTTTGTGATTGCC 1599  
  
Qy 538 ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg 557  
|||||  
Db 1600 ACAACACAGACAGCTGAGTGTCTTCAACCCGGTCTTTAAGCTCCTTGAACCTCACCTCCGT 1659  
  
Qy 558 GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeu 577  
:::  
Db 1660 GATACGATGAATATCAATGCACCTGTAGGCAATCTTGATCAATGGTGGTATATTT 1719  
  
Qy 578 GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp 597  
|||:::  
Db 1720 GAAATCACTGTGTTCTCTTAATACGCCATGGAGATGTCTTTCATTACAAAAC 1779  
  
Qy 598 ---TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616  
|||  
Db 1780 CACTGGACCTTCCCTGACCAAGCAATTACCAGCAGAACTTAAAGAGAGGGATGCCGTT 1839  
  
Qy 617 GluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal 636  
|||||  
Db 1840 GAGGATCCGAAGCACCACACCGGATTACGTCTGAGGATAAAAGACTATCCTTACGCAGTG 1899  
  
Qy 637 AspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyr 656  
|||||  
Db 1900 GATGGCTTGAGGTTGGTATGCTATTGAATCATGGTCCGAGACTACATTTTCTTGTTC 1959  
  
Qy 657 TyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeu 676  
|||||  
Db 1960 TACAAGATAGAGGAGGATATCCAAACCGACACAGAGCTCCAAGCCTGGTGAAGAGGTG 2019  
  
Qy 677 ArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrVal 696  
|||||  
Db 2020 CGCGAGGAAGGTCATGGAGACAAAAGTCAGAACCATGGTGGCTAAATGCAACCCGT 2079  
  
Qy 697 GlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAla 716  
:::  
Db 2080 GAAGAACTTGTGAGTCTTGCAACCATCATTTATTTGGTGGCTTCTGCTCTTCATGCAGCT 2139  
  
Qy 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736  
|||||  
Db 2140 GTTAACTTCGGACAGTATCCAGTTGCTGGGTACCTCCAAACAGACCGACTATAAGCCGT 2199  
  
Qy 737 AsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLys 756  
:::  
Db 2200 CAGTACATGCCAAAGGAAACACTCCAGAGTTTGAAGAACTTGAGAAGAATCCTGTATAA 2259  
  
Qy 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776  
|||||  
Db 2260 GTGTTTTGAAGACCATCACAGCTCAGCTTCAGACACTTCTAGGGATATCTCTGATTGAG 2319  
  
Qy 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrp 796  
|||||  
Db 2320 ATTCTCTTACTCATCTTAGCGACGAGGTCTATTTTGGACAGAGAGATTCTAAAGAATGG 2379  
  
Qy 797 ThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIle 816  
:::  
Db 2380 GCGGCTGAGAAAGAACGTTTGGAGCGTTCGAGAAGTTTGGAGAGAAAGTAAAGGAGATT 2439  
  
Qy 817 GluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProVal 836  
|||  
Db 2440 GAGAAGAACATTGATGAGAGGAACCGACGACGAGACTCTCAAGAACAGGACTGGTTTGGTT 2499  
  
Qy 837 LysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysGlyIle 856  
|||:::  
Db 2500 AAGATGCCATACACTTATTGTTTCCGAGCAGTGAAGCGGAGTCAACCGCAGGGAATT 2559  
  
Qy 857 ProAsnSerValSerIle 862  
|||  
Db 2560 CCAAAATAGCGTCTCTATC 2577

RESULT 6

ADA67958  
ID ADA67958 standard; DNA; 2580 BP.  
XX  
AC ADA67958;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Arabidopsis thaliana gene, SEQ ID 206.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
DR WPI; 2003-175290/17.  
XX  
Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.  
Claim 6; SEQ ID NO 206; 899pp; English.  
XX  
The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 2580 BP; 778 A; 541 C; 616 G; 645 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 4.89e-293 Length: 2580  
Score: 3202.50 Matches: 595  
Percent Similarity: 82.79% Conservative: 122  
Best Local Similarity: 68.71% Mismatches: 138  
Query Match: 70.63% Indels: 11  
DB: 8 Gaps: 7  
  
US-10-731-642A-1 (1-862) x ADA67958 (1-2580)  
Qy 1 MetPheLeuGluLysIleValAspAlaIleThrGly-----LysAspAspGlyLys 17  
|||||  
Db 1 ATGTTCCGAGAA---CTTAGGATCTGCTCACCGCGCGGAAATGAGACGACGAAG 57  
|||||  
Qy 18 LysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsn 37  
|||||  
Db 58 AAGTGAAAGGAACGGTGTCTTGATGAAGAAGAACGTCCTCGATTCAACGATTTCAT 117  
|||||  
Qy 38 AlaSerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIle 57  
|||||  
Db 118 GCTTCGTTTCTCGATCGTCTTCATGAATTTCTCGGAACAACAAATCACTTCTCGTCTTGA 177  
|||||  
Qy 58 SerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyr 77  
|||||

Db 178 AGCTCTGATGTTACTGATTCAGAAAAACGGTTCTAAAGGCAAACTAGGGAAGGCTGTCTCAC 237

Qy 78 LeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgVal 97

Db 238 TTGGAGGATTGGATCACAAACAATCACGTCGTAAACCGCAGGCGAATCCGCTTTCAGGTC 297

Qy 98 ThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeu 117

Db 298 ACGTTCGATTAC--GAAACCGATTTCGGTTACCTGGAGCAATCTTGATCAGAAACAGC 354

Qy 118 HisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLys 137

Db 355 CATTTTCAGTGAGTTCTTCTCAAAAGTCTCACACTTGAAGACGTTCCAGGCCATGGCAGA 414

Qy 138 ValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIle 157

Db 415 GTCCATTACATCTGTAATTCTTGGATTACCTGTAAACACTACACTACAGACCGAGTC 474

Qy 158 PhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArg 177

Db 475 TTCTTCTCCAAACAAGACTTATCTTCCACATGAACAACACCAGCGCGCTCAAGTATAGA 534

Qy 178 GluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArg 197

Db 535 GAAGAGAGCTAGTGAGTTTGAGAGGAACCGCGGAAGGAGCTTAAGGAATGGGACAGA 594

Qy 198 ValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSer 217

Db 595 GTATATGACTATGCTTACTACATGATTTAGGCGTCCCAACCAAGAAC-----CCA 645

Qy 218 ArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArg 237

Db 646 CGGCCCTGTACTTGGAGGGACACAGGAGTAGTATCCTTACCCAGAAGAGGAACCCGGGCGG 705

Qy 238 LysProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAsp 257

Db 706 AAACCAACTAAAGAAGATCCTCAAACCGAGAGCAGGCTACCGATCACATCGAGCCTAGAC 765

Qy 258 IleTyrValProArgAspGluArgPheGlyHisIleLysLysLeuSerAspPheLeuThrPhe 277

Db 766 ATATATGTTCCACGAGATGAGAGATTTGGACACTTGAAGATGTCTGATTTCTTGCTTAT 825

Qy 278 AlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThr 297

Db 826 GCTCTAAAGCGATTGCTCAGTTCTCCAACTGCACCTTGAGGCTGTATTTCGACGATACT 885

Qy 298 HisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeu 317

Db 886 CCTAAAGAGTTTGATTCTTTTGAAGATGTTCTTAAGATCTATGAAGAAGGAATCGATCTA 945

Qy 318 ProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGlu 337

Db 946 CCAAAACCAAGCTTTGATTGATAGTATCGTTAAGAAATATACCGCTTGAGATGTTAAAGGAG 1005

Qy 338 LeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGlu 357

Db 1006 ATATTCAGAACAGATGGCCAGAAAATTCCTTAAGTTTCCAGTGCCTCAGGTCAATCAAAGAG 1065

Qy 358 AspLysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsn 377

Db 1066 GACAAAACTGCATGGAGAACAGATGAGGAATTTGCTAGAGAAATGTTGGCTGGACTAAAC 1125

Qy 378 ProValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIle 397

Db 1126 CCTGTTGTTATTCAACTTCTTAAGGAGTTTCTCCAAAGAGTAAGCTTGACAGTGAATCA 1185

Qy 398 TyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeu 417

Db 1186 TACGGTAACCAAGAACAGTACAATCACTAAAGCCACATAGAACACAATTTGGATGGACTC 1245

Qy 418 ThrIleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisAspIleLeu 437

Db 1246 ACTGTTGAAGAGGCTCTGGAGAAGGAGAGGTTGTTTATATTAGACCACCATGACACACTG 1305

Qy 438 MetProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThr 457

Db 1306 ATGCCATACTTGGGACCGCGTAAACACCACCAG--ACCAAGACTTATGCAAGCAGGACA 1362

Qy 458 LeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuPro 477

Db 1363 CTTCTGTTCTTGAAAGATGATGGGACCTTGAAGCCGTTGGTGATAGAGCTGAGCTTGCCT 1422

Qy 478 HisProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGly 497

Db 1423 CATCCTAATGGAGACAAATTTGGAGCAGTGAGTGAAGTATATACGCTGGT--GAAGGT 1479

Qy 498 ValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyVal 517

Db 1480 GTCTACGACTCGCTATGGCAGTTGGCTAAGGCTTTTGTGCGTGTAAATGACTCCGGAAT 1539

Qy 518 HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluPropheValIleAla 537

Db 1540 CATCAGCTTATTAGCCACTGGATGCAAAACACACGCATCGATTGAACCGTTTGTGATTGCC 1599

Qy 538 ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg 557

Db 1600 ACAAAACAGACAGCTGAGTGTTCTTCACCCGGTCTTTAAGCTCCTTGAACCTCACTTCCGT 1659

Qy 558 GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeu 577

Db 1660 GATACGATGAATATCAATGCATTCGTAGGCAAAATCTTGATCAATGGTGGTATATTT 1719

Qy 578 GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp 597

Db 1720 GAAATCACTGTGTTTCTCTTAAATACGCCATCGGATGTCTATCTTCATTACAAAAAC 1779

Qy 598 ---TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaVal 616

Db 1780 CACTGGACCTTCCCTGACCAAGCATTACCAGCAGAACTTAAAAAGAGAGGGATGGCCGTT 1839

Qy 617 GluAspSerSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaVal 636

Db 1840 GAGGATCCAGAAGCACCAACACCGGATTACGTCTGAGGATAAAAGACTATCCTTACGCAGTG 1899

Qy 637 AspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyr 656

Db 1900 GATGGCTTGAGGTTTGGTATGCTATTTGAATCATGGGTCCGAGACTACATTTTCTTGTTC 1959

Qy 657 TyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeu 676

Db 1960 TACAAGATAGAGGAGGATATCCAAACCGACACAGAGCTCCAAGCTGGTGGAAGGAGTG 2019

Qy 677 ArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrVal 696

Db 2020 CGCGAGGAAGTTCATGGAGACAAAAAGTCAGAACCATGGTGGCTAAAAATGCAAAACCGT 2079

Qy 697 GlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAla 716

Db 2080 GAAGAACTTGTGAGTCTTGACCATCATTTATTTGGGTGGCTTCTGCTCTTCATGCAGCT 2139

Qy 717 ValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArg 736

Db 2140 GTTAACTTCGGACAGTATCCAGTTGCTGGTACCTCCCAACACAGACCGACTATAAGCCGT 2199

Qy 737 AsnPheMetProGluProGlySerProGluTyrGluGluLysThrAsnProAspLys 756

Db 2200 CAGTACATGCCAAAGGAAAAACACTCCAGAGTTTGAAGAACTTGAGAAAGAAATCCTGATAAA 2259

Qy 757 ValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGlu 776

Db 2260 GTGTTTTTGAAGACCATCACAGCTCAGCTTCAGACACTTCAGGGATATCTCTGATTGAG 2319

Qy 777 IleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrp 796

Db 2320 ATTCTCTACTCATTTCTAGCGAGGCTCTATTTGGGACAGAGAGATTCTTAAAGAAATGG 2379





QY 64 ----- 64  
Db 853 ATTTTGTAGAAATAACATGTAAAAATGCAGTGACCATCTGTTAGTGATGATATTGAACTTG 912  
QY 65 -----AlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAs 80  
Db 913 TGTGCCCTTTGTAGCAATGGTTACAGGGGAAACTTGGGAAACCAGCATACTTGGAGA 972  
QY 80 nTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAs 100  
Db 973 CTGGATTACCAAAATTACTTCTTTAAACCGCTGGCGAGTCTGCATTCAAGGTCACGTTCCGA 1032  
QY 100 pTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSe 120  
Db 1033 CTGG---GATGAGGAGATTGGAGAGCCAGGGGCATTCTAATATTAGAAACAATCACCACAG 1089  
QY 120 rGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPh 140  
Db 1090 TGAGTTTACCTCAGGACTCTCAGCTCTTGAAGATGTTCTGGACGTGGCAGAAATTCACIT 1149  
QY 140 eValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAl 160  
Db 1150 TGTTTGTAAATTCCTGGGTCTACCCCTGCTAAGCACTACAAAACACTGACCGTGTCTTCTTCCAC 1209  
QY 160 aAsn----- 161  
Db 1210 TAATCAGGTAAGACTAAATTTGCTTGATAGTAGGAGAGTCTGCTGTGGCATTTGTGGCCCAT 1269  
QY 162 -----GlnAl 163  
Db 1270 TGAGCTTAGGCAAGGAGAAATGTCTGTCTAAAGGAATGTGTTTATTATCTGCTGCAGAC 1329  
QY 163 aTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValTh 183  
Db 1330 ATATCTTCCAAGTGAAACACCCAGGCGCACTGCGCAAGTACAGAAAAGGGGAACTGGTGAA 1389  
QY 183 rLeuArgGlyAspGlyThrGlyLysLeuGluGluTyrAspArgValTyrAspTyrAlaTy 203  
Db 1390 TCTGAGGGGAGATGGAACCGGAGAGCTTAAAGGAATGGATCGAGTGTATGACTATGCTTA 1449  
QY 203 rTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGl 223  
Db 1450 CTATAATGATTTGGGGAAGCCAGACAGGATCTCAAATATGCCCGCCCTGTGCTGGGAGG 1509  
QY 223 ySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys----- 241  
Db 1510 ATCTGCAGAGTATCCTTATCCAGGAGGGGAAAGAACTGGTAGACCACCATCTGAAAAAGG 1569  
QY 241 ----- 241  
Db 1570 TAGATAATTGATACACAAATTCATATTGTTTCTCATGCTTTTATCATATAAAAGGATGAATA 1629  
QY 242 -----ThrAspProAsnSerGluSerArgIleProLe 252  
Db 1630 TGATTGATTCTGCTCTCTTTTAAATTAACAGATCCCAAACTGAGAGCAGATTGCCACT 1689  
QY 252 uLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSe 272  
Db 1690 TGTGATGAGCTTAAACATATATGTTCCAAGAGATGAACGATTTGGTCACCTGAAGATGTC 1749  
QY 272 rAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPheLysAl 292  
Db 1750 AGACTTCCTGGCTTATGCCCTGAAATCCATAGTTCAATTCTCTCTCCTGAGTTTGAGGC 1809  
QY 292 aLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGl 312  
Db 1810 TCTATGTGACATCACCCCAATAGTTTGGACAGCTTCCAAGATGTATTAGACCTCTACGA 1869  
QY 312 uGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProLe 332  
Db 1870 AGGAGGAATCAAGGTCCCAGAGGGCCCTTTACTGGACAAAATTAAGGACAAACATCCCTCT 1929

QY 332 uGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrPr 352  
Db 1930 TGAGATGCTCAAGGAACATTGTTTCGTACCGATGGGAACATCTCTTCAAGTTCCCAATGCC 1989  
QY 352 oGlnValIle-Gln----- 356  
Db 1990 CCAAGTCATCAAAAGGTACTGTCATACATCTAACAATCTTGTAAATCTTTGAAGCCAGATTAT 2049  
QY 357 -----GluAspLysThrA 361  
Db 2050 ATATTTATTTTTCATAAAATTTGATGACGTTTTTATCATGCTGGAGCAGAGATAAGTCTG 2109  
QY 361 laTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleI 381  
Db 2110 CATGGAGGACTGACGAAGAATTTGCTAGAGAAATGCTGGCTGGACTCAACCCAGTTGTCA 2169  
QY 381 leSerArg----- 383  
Db 2170 TCCG-TCTACTCCAAGTAAACTACAGCTTCCTTTCAAATAAATTTTAATGCCCTGTTGT 2228  
QY 383 ----- 383  
Db 2229 TTTCTGAGAAAAATGGAACCTTGGAAAGGCTTCAGACTTTGTTTCTTCTTCCCTCCATCTAC 2288  
QY 384 -----LeuGlnGluPheProp 389  
Db 2289 TGTTCTAGCTCTTTTCTGATAATTATTGGCTCTTTCTACTTTTGTGTAAGGAGTTTCTCTC 2348  
QY 389 roLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluG 409  
Db 2349 CAAAAAGCAAGCTGGATCCTGAGATTATGGCAACCAAAACAGTTCAATAACCAAGAAC 2408  
QY 409 lnIleGluAspLysLeuAspGlyLeuThrIleAspGluAla----- 422  
Db 2409 ACATAGAGAATCACCTGGATGACCTTACTATATAAACGAGGT-AAACGCTCTTAGGTTCCGTT 2467  
QY 422 ----- 422  
Db 2468 CTTTCAAACATAAATTTTCAATGTGACATGTTAAATTTTTCATTTGCAATGGAAACACAAGCCAT 2527  
QY 423 -----IleLysThrAsnArgLeuPheIleLeuA 432  
Db 2528 AGTAAC TGAAAAATGGTGTCTTTTACTAGGCAATGGAGAAGAGAGGCTATTCATATTAG 2587  
QY 432 snHisHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysT 452  
Db 2588 ATCACCATGATGTTTTCATGCCATACCTGAGGAGGATAAACACA---ACTTCCACGAAAA 2644  
QY 452 hrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaI 472  
Db 2645 CTTACGCTCAAGGACTCTCTCTTCTTGAAAGACGACGGAACCTTTGAAGCCACTGGCGA 2704  
QY 472 leGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrT 492  
Db 2705 TTGAATTGAGCCTACCACATCCTAATGGGATAAAATTCGGAGCTGTCAACAAAAGTATACA 2764  
QY 492 hrProAlaAspGlnGlyValGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlav 512  
Db 2765 CACCAGCTGAAGATGGCGTTGAAGGTTCCATTTTGGCAGCTGGCTAAAAGCTTATGCTGCTG 2824  
QY 512 alaAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeu----- 525  
Db 2825 TGAATGACTCTGGCTATCATCAGCTCCTCAGCCACTGGTA-CGTAATCTCCCAAAGGAAA 2883  
QY 525 ----- 525  
Db 2884 GTGCGTACAGTTGGGGCGTAAATCTGAAGCGGGTTATGAATATCTTTTGATGTTGGTTGCA 2943  
QY 526 -----AsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerA 544  
Db 2944 GGTGAATACACATGCTGCAATTGAGCCATTGTTGATTGCAACCAACAGGAGCTCAGTG 3003  
QY 544 laLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnA 564



QY 38 AlaSerValLeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIle 57  
Db 64 GCCTCTCTTGATCGTCAATGAGCTTCTTGGTCGTGCTCTCTCCACCTCATC 123  
QY 58 SerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyr 77  
Db 124 AGCTCTCACCAACCCGACCCGCCCAATGAGAAGAGAGGAGACTTGGAAAAGCAGCACAT 183  
QY 78 LeuGluAsnTrpLeuThrAsn---SerThrProIleAlaAlaGlyGluSerAlaPheArg 96  
Db 184 CTGGAATAATGGGTAAACAAAAATAAAACGTCAGTAACCGCTGAGGAAACTGCGTTTGGGA 243  
QY 97 ValThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsn 116  
Db 244 GTAACGTTTGATTGG---GACGAGTCAATGGGACCACCGGCTGCATTGTGTATCAAGAAC 300  
QY 117 LeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGly 136  
Db 301 CACCACCATAGTCAATTCTACCTTAAGTCCCTCACCTCCCGGGCTTCCCTGAT---GGC 357  
QY 137 Lys-----ValHisPheValCysAsnSerTrpValTyrProAlaAsnLys 151  
Db 358 GAAGGTGGTGCCACTCGGATACATTTCACTGTCAATTCTTGGATTACCCGAATCATCGA 417  
QY 152 TyrLysSerAspArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAsp 171  
Db 418 TACCGCTCCGACCGCGTCTTCTCTCTAAACAGGCATATCTTCCAAGTGAACACCCGGAG 477  
QY 172 ThrLeuArgLysTyrArgGluAsnGluLeuValThrLeuArgGly---AspGlyThrGly 190  
Db 478 CTAATCAAAAGAGCTAAGAGAAGAGAGCTAAAGAAATCTAAGAGGCAATGAGAAAGGAGGA 537  
QY 191 LysLeuGluGluTrpAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspPro 210  
Db 538 GAATTCAAAGAATGGACAGAGTTTACGACTACGCTTATTACACGACTTGGGTGCTCCT 597  
QY 211 AspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrPro 230  
Db 598 GACAAAGGTCTGACTCAGTTTCGTCCGGTCTTGGCGGTTACCTGAGCTGCCTTATCCT 657  
QY 231 ArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsnSerGluSerArgIle 250  
Db 658 CGCCGTGGCAAAACCGGCCGTAAATCCACCAAAATCAGACCCCTAAGTCTGAAAGCAGGCTG 717  
QY 251 ProLeuLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLys 270  
Db 718 GCCTTTACTA---AACCTAAACATATACGTGCCAAGGACGAGCGATTAGCCATGTGAAG 774  
QY 271 LeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuLeuProGluPhe 290  
Db 775 TTTTTCAGACTTCCTCGCTTATGCATCAAGTCCGTGACTCAAGTGTGTCTCCCTGAGATC 834  
QY 291 LysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeu 310  
Db 835 GCCTCTGTGGCACAAGACCATCAACGAGTTTGACTCTCTTCGAAGATGTTTTTCACCTC 894  
QY 311 TyrGluGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIle 330  
Db 895 TATGACGGTAGATTAAAGCTCGCCAAATGGTCACACCATTCTTAAGCTCCGTGATGTTATC 954  
QY 331 ProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrPro 350  
Db 955 CCGTGGGAGATGTTTAGAGAGCTAGTTCCGCAACGACGAGAACCGGTTCTTGAAGTATCCC 1014  
QY 351 ThrProGlnValIleGlnGluAspLysThrAlaTyrArgThrAspGluGluPheGlyArg 370  
Db 1015 TTGCCTGACATCCTCAAAGAGAGCAGATCGGCTTGGAGGACTGACGAAGAGTTTGCTCGA 1074  
QY 371 GluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGlnGluPheProProLys 390  
Db 1075 GAAATGCTGGCCGGTCTTAATCCGGTGGTGATTAGCCGTCTTCAGGAATTTCCACCAAG 1134

QY 391 SerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIle 410  
Db 1135 AGCTGTCTGGACTCTGCAAAGTATGGAACCAACACTCTTCCATACGAACAGAGCACATA 1194  
QY 411 GluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPheIle 430  
Db 1195 GAATCAAAACATGAACGGCCTCAATGTCCAAGAAGCTTTGGAACAGATAAAGCTATACATA 1254  
QY 431 LeuAsnHisHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThr 450  
Db 1255 TTGGATCATCAGCAGCGCATTTGATGCTTACCTGACACGGATAAAC---TCAACAAACACT 1311  
QY 451 LysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSer 470  
Db 1312 AAAACCTATGCGACCCGAAACCCCTGCTGTGTCTTCAAGCAGACGGAACACTGAAGCCTCTC 1371  
QY 471 AlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysVal 490  
Db 1372 GCCATAGAGCTGAGTCTTCCACACGCAAGGCGAATCATATGGATCGGTCAAGAAAGTT 1431  
QY 491 TyrThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAla 510  
Db 1432 TTCACACCAGCAGAGAAAGGTGTCGAGGGATCGGTTTGGCAACTTGTCTAAGGCTTATGCT 1491  
QY 511 AlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAla 530  
Db 1492 GCGGTCAATGACTCTGGTTATCATCAGCTTATAAGCCATTGGTTGCAAAACGCATGCGGTG 1551  
QY 531 IleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLys 550  
Db 1552 ATTGAACCGTTTCATAATCGCGTCCAATAGGCAGCTCAGCGTGGTCCATCCGATCCATAAA 1611  
QY 551 LeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeu 570  
Db 1612 CTTTACATCCTCATTTCCGTGACACTATGAACATCAACGCATTAGCGCGTCATGTACTC 1671  
QY 571 IleAsnGlyGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMet 590  
Db 1672 ATAAACTCAGACGGAGTTCTTGAGAGAAACAGTCTTCCCTAGTCGATACGCCATGGAATG 1731  
QY 591 SerAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIle 610  
Db 1732 TCCTCTCAATTACAAAGAATTGGGTTTTCACCGAGCAGGCTCTCCCAAAGACCTCCTC 1791  
QY 611 LysArgGlyValAlaValGluAspSerSerSerProLeuGlyIleArgLeuLeuIleGln 630  
Db 1792 AAACGAGGAGTTGCTGTTGAAGATCCAAACAGTGAGAACGGCGTTAAGCTTCTGTATCGAA 1851  
QY 631 AspTyrProTyrAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThr 650  
Db 1852 GATTACCCGTTTTCGGTTCGACGGTTTAGAGATTTGGTCAGCGATCAAAACATGGGTCA 1911  
QY 651 GluTyrCysAsnTyrTyrTyrLysSerAspAspAlaValGlnLysAspThrGluLeuGln 670  
Db 1912 GAGTACTGCACATTCTACTACAATAATGACAAAACCGTCCAAAACGGATACAGAGATCCAA 1971  
QY 671 AlaTrpTrpLysGluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrp 690  
Db 1972 TCATGGTGGACCGAGCTCCGAAACCAAGGCCACGGCGACAAACGACACGAGTATGGTGG 2031  
QY 691 ProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAla 710  
Db 2032 CCTTCGATGCAAAACCCCGCAGCACCTTAATCGAAAACCTGCACCATCATCTGGATCGCC 2091  
QY 711 SerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsn 730  
Db 2092 TCTGCTCTTCAGCAGCAGTAATAATTTCGACAGTACCCCTTACGCCGGTCTTCTCCCTAAC 2151  
QY 731 ArgProThrLeuSerArgAsnPheMetProGluProGlySerProGluTyrGluLeu 750  
Db 2152 CGTCTACCGTCAGCCCGCGGTATTATGCCTGAACCCAGGTACGGATGAGTATGCTGAGCTG 2211  
QY 751 LysThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeu 770



Db 2212 GAGGAAGATGCTGACGTAGCGTTCCTTGAAGACGATCAGCCGCGAGTTACAGACTCTACTT 2271  
Qy 771 GlyIleSerLeuIleGluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGln 790  
Db 2272 GGTATCTCCATCATAGAGATATTGTCTATGCATTCAACGGACGAGACTACTTAGGGCAA 2331  
Qy 791 ArgGluSerProGluTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGly 810  
Db 2332 AGAGATTACCGGAATTGGACGGCGGATGATGAGCCTTTGGAGGCGTTTAAGCGGTTTGGG 2391  
Qy 811 LysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLys 830  
Db 2392 AAAGAACTTGAGCTGATAGAGAACAATATTATACGAAGAACAATGACAAGAGGTTCAAG 2451  
Qy 831 AsnArgSerGlyProValLysValProTyrThrLeuLeuPhePro----- 845  
Db 2452 AACAGAACCGGACCGGTTAACATACCGTACACATTGTTGTACCGGAATACTACGGATTAT 2511  
Qy 846 ThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862  
Db 2512 ACGAGAGAAGGTGGGATTACTGGGAAAGGGATCCCGAACAGTGTCTCAATC 2562  
RESULT 9  
AAL57712  
ID AAL57712 standard; cDNA; 2929 BP.  
XX  
AC AAL57712;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Balsam pear (Momordica charantia) lipoxxygenase isozyme 2 cDNA.  
XX  
KW Lipoxxygenase; hydroperoxidation; polyunsaturated fatty acid; plant;  
KW fatty acid metabolite synthesis; signal molecule; growth regulation;  
KW development regulation; plant development; wound response;  
KW genetic mapping; hyperoxidation catalysis; Balsam pear; gene; ss.  
XX  
OS Momordica charantia.  
XX  
FH Key Location/Qualifiers  
FT CDS 12..2654  
FT /\*tag= a  
FT /product= "Balsam pear lipoxxygenase 2"  
XX  
PN US2003074693-A1.  
XX  
PD 17-APR-2003.  
XX  
PF 29-JAN-2002; 2002US-00059909.  
XX  
PR 10-FEB-1999; 99US-0119597P.  
PR 09-FEB-2000; 2000US-00501422.  
XX  
PA (CAHO/) CAHOON E B.  
PA (KINN/) KINNEY A J.  
PA (KLEI/) KLEIN T M.  
PA (LEEJ/) LEE J.  
PA (PEAR/) PEARLSTEIN R W.  
PA (RAFA/) RAFALSKI J A.  
PA (SHEN/) SHEN J B.  
PA (THOR/) THORPE C J.  
PA (TING/) TINGEY S V.  
PA (WENG/) WENG Z.  
XX  
PI Cahoon EB, Kinney AJ, Klein TM, Lee J, Pearlstein RW;  
PI Rafalski JA, Shen JB, Thorpe CJ, Tingey SV, Weng Z;  
XX  
DR WPI; 2003-567325/53.  
DR P-PSDB; AAO27492.  
XX  
PT New isolated polynucleotides encoding plant lipoxxygenases, useful in  
genetic mapping, particularly in catalyzing hyperoxidation of

PT polyunsaturated fatty acids.  
XX Claim 6; Page 22-23; 36pp; English.  
PS  
XX This invention relates to novel nucleotide sequences which encode  
CC proteins which have lipoxxygenase activity. Lipoxxygenases are membrane  
CC bound ubiquitous enzymes which catalyse the hydroperoxidation of  
CC polyunsaturated fatty acids in the first step of fatty acid metabolite  
CC synthesis. Products of this pathway are found as signal molecules  
CC involved in growth and development regulation. A knowledge of the amino  
CC acid sequence of lipoxxygenases may allow the understanding of plant  
CC development and wound response. The polynucleotides, polypeptides and  
CC lipoxxygenases of the invention may therefore be useful in genetic mapping  
CC and particularly for catalysing hydroperoxidation of polyunsaturated  
CC fatty acids. The present sequence is the cDNA sequence which encodes the  
CC Balsam pear (Momordica charantia) lipoxxygenase protein 2 of the invention  
XX  
SQ Sequence 2929 BP; 910 A; 587 C; 662 G; 770 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 6.92e-276 Length: 2929  
Score: 3022.50 Matches: 554  
Percent Similarity: 80.99% Conservative: 132  
Best Local Similarity: 65.41% Mismatches: 156  
Query Match: 66.66% Indels: 5  
DB: 9 Gaps: 4  
US-10-731-642A-1 (1-862) x AAL57712 (1-2929)  
Qy 16 GlyLysLysValLysGlyThrValValLeuMetLysLysAsnValLeuAspPheThrAsp 35  
Db 126 GGGAAAGAAGATCAAAGGGACGCGTGTCTTATGAGAAGCAATGTTTGGACTTCACCGAA 185  
Qy 36 IleAsnAlaSerValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGlu 55  
Db 186 TTTCAATTCCTCACTTCTTGACGGCGTCACTGAGCTCTTGGCGGCGGAATTTTCATTGCAA 245  
Qy 56 LeuIleSerSerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAla 75  
Db 246 CTTATCAGTGCTACTCAGCT-----TCCAACGACTCGCGAGGGAAGTTGGAAAGGGG 299  
Qy 76 AlaTyrLeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPhe 95  
Db 300 GCGTTCTGGAGAGGTGGCTGACTTCAGTTCGCCCACTGTTCCGCTGGAGAGTCTGTGTTT 359  
Qy 96 ArgValThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleLys 115  
Db 360 CAACTGAACCTTTGATTGG---GAAGAGAACCTTTGGATTTCAGGAGCTTCTTCATAAAA 416  
Qy 116 AsnLeuHisPheSerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis 135  
Db 417 AATGGGCACACCAGTGAGTTCTCTCAAGTCTGTAACCTCGAGGATGTTCTCGGCTTT 476  
Qy 136 GlyLysValHisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAsp 155  
Db 477 GGAAGGGTCCATTTTGACTGCAACTCATGGGTTTACCCCTTCTCGAAGATACAAGAAAGAT 536  
Qy 156 ArgIlePhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLys 175  
Db 537 CGCATTTTCTTTGCCAACCATACATGCCTTCCAATCGATACACCGGATTCACCTTCGTAAG 596  
Qy 176 TyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGlyLysLeuGluTrp 195  
Db 597 TATAGAGAGGAGGAGTTGTTGAACCTCAGAGGAGATGGAACAGGAGCGCTAAAGATGG 656  
Qy 196 AspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAsp 215  
Db 657 GATAGAATTATGACTATGATGTTTACAACGACCTCTGTGATCCAAATGGTGGTCCCTAAC 716  
Qy 216 LeuSerArgProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThr 235  
Db 717 CTTGTTGTCCTATTCTTTGGAGGAGTGATCAGTACCCCTTACCCTTCGTAGAGGGAGACA 776



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FT XX /product= "LBLOX"
PN DE19950921-A1.
XX
PD 26-APR-2001.
XX
PF 21-OCT-1999; 99DE-01050921.
XX
PR 21-OCT-1999; 99DE-01050921.
XX
PA (BADI ) BASF AG.
XX
PI Kindl H, May C, Feussner I;
XX
DR WPI; 2001-274658/29.
DR P-PSDB; AAB86036.
XX
PT New isolated nucleic acid encoding sequence that targets proteins to
PT lipid bodies, useful for producing transgenic plants for lipid and fatty
PT acid production.
XX
PS Claim 1d; Page 14-18; 30pp; German.
XX
CC This invention describes a novel isolated nucleic acid sequence (I),
CC encoding a polypeptide, comprising a sequence (Ia) involved in fatty acid
CC or lipid metabolism, and a targeting sequence (Ib). (I) are used to
CC produce oil-producing transgenic plants or eukaryotic microorganisms, for
CC production of lipids or derived fatty acids. This sequence encodes a
CC Cucumis sativus (cucumber) LBLOX protein which is described in the method
CC of the invention
XX
SQ Sequence 2964 BP; 988 A; 516 C; 583 G; 877 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,64e-265 Length: 2964
Score: 2911.00 Matches: 534
Percent Similarity: 78.65% Conservative: 140
Best Local Similarity: 62.31% Mismatches: 175
Query Match: 64.20% Indels: 8
DB: 4 Gaps: 6

US-10-731-642A-1 (1-862) x AAF88022 (1-2964)
QY 6 ileValAspAlaIleThrGlyLysAspGlyLysLysValLysGlyThrValValLeu 25
Db 135 ATTTAGATAGAGTTTCAGTCTT---GGAGGAAACAAATCAAGGAAAGTGATCTT 191
QY 26 MetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAspGlyValLeu 45
Db 192 ATGAGAAGCAATGTTTGATTTCACTGAATTCATTCCAATCTTCTTGATAACTTCACT 251
QY 46 GluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAlaAspProAla 65
Db 252 GAGCTCTTGGTGGTGGTCTTTCTTCCAACTCATTAGTGCCACTCATACT-----TCA 305
QY 66 AsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeuThrAsnSer 85
Db 306 AATGACTCAAGAGGAAAGTTGGGAACAAGGCATATTTGGAGAGGTGGCTAACTTCAATC 365
QY 86 ThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAspGluGlu 105
Db 366 CCACCACTGTTTGGTGGAGAAATCAGTGTTCAAATCAACTTTTCAATGG---GATGAAAT 422
QY 106 PheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPheLeuLys 125
Db 423 TTTGGATTTCCAGGAGCTTCTTCATAAAAAATGGACATACAAAGTGAATCTTCTCTCAA 482
QY 126 SerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCysAsnSerTrp 145
Db 483 TCTCTCACTCTTGATGATGTTCTTGCTATGGCAGAGTCCATTTTGATGCAATCTTGG 542
QY 146 ValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGlnAlaTyrLeu 165
Db 146 ValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGlnAlaTyrLeu 165

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Db 543 GTTTACCCCTTCTGGAAGATACAAAGAAAGATCGCATTTTCTTTGCCAATCATGTTTATCTT 602
QY 166 ProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValThrLeuArg 185
Db 603 CCAAGTCAAACACCAACCTCTTCGTAGTATAGAGAGGAAGAATTGTGGAATTGAGA 662
QY 186 GlyAspGlyThrGlyLysLeuGluTyrAspArgValTyrAspTyrAlaTyrTyrAsn 205
Db 663 GGAGATGGAACAGGAGAAAGGAATGGGATAGAATTATGACTATGATGTTTATAAT 722
QY 206 AspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSer 225
Db 723 GACATTGCTGACCCCTGATGTTGGTGAT-----CATCGTCTTATTTCTCGGTGGGACGACC 776
QY 226 GluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsn 245
Db 777 GAATATCCTTACCCTCGTAGGGAAGAACAGGACGACCAAGATCAAGAAAGAGACCACAAT 836
QY 246 SerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArgAspGluArg 265
Db 837 TATGAGAGCAGATTGTCCCAATAATGAGCTTAGACATCTATGTACCAAAAGATGAAAAC 896
QY 266 PheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeu 285
Db 897 TTGGGCATTTGAAGATGTCAGATTTCCTTGGTTATACATATAAAGCACTTTCGATATCA 956
QY 286 LeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGlu 305
Db 957 ATCAAAACCAGGACTTCAATCCATATTTGATGTAACTCCCAATGAATTTGACAAATTTAAA 1016
QY 306 AspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAla 325
Db 1017 GAAGTTGATAAATCTCTTTGAGAGAGGTTTTTCCCATTCCATTAAAT---GCTTTTAAGACC 1073
QY 326 IleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGly 345
Db 1074 CTCACCTGAGGACCTCACTCCACTTTGTTTCAAAGCACTCGTGAGGAATGATGGTGAAAA 1133
QY 346 LeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAsp 365
Db 1134 TTCTCTCAAATTTCTTACTCCCGAAGTTGTCAAAGATAATAAAATAGGATGGAGCACTGAT 1193
QY 366 GluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGln 385
Db 1194 GAAGAATTGCAAGAGAAATGTTAGCAGGACCCCAATCCTCTTATTGATTCGTCTCTTGA 1253
QY 386 GluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIle 405
Db 1254 GCTTTTCCACCAACAAGTAGCTTGACCCCAATGTTTATGGGAATCAAAACAGTACCATC 1313
QY 406 ThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThr 425
Db 1314 ACTGAAGAACACATAAAGCATGGTTTAGATGGTCTTACGGTTGATGAGGCAATGAAGCAA 1373
QY 426 AsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyrLeuArgArgIleAsn 445
Db 1374 AACAGGCTCTACATAGTGGATTTCCATGATGCATTAATATGCCCTATCTTACAAGGATGAAT 1433
QY 446 ThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGly 465
Db 1434 ---GCAACATCAACAAAAACATATGCCACAAGAACATTTGCTCTTTTGAAGATGATGGG 1490
QY 466 ThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGly 485
Db 1491 ACTTTGAAGCCATTGGTTATTGAGTTAGCTTGCCACATCTCTCAAGGAGATCAACTTGGT 1550
QY 486 AlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeu 505
Db 1551 GCCATTAGCAAACTATACTTTCCAGCTGAAAATGGAGTTCAAAAATCCATTGGCAATTG 1610
QY 506 AlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeu 525
Db 1611 GCTAAAGCTTATGTAACTGTTAATGATGTTGGCTACCATCACTTATTAGTCATTGGTTG 1670

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Qy 526 AsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeu 545  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1671 CATACTCATGCTGTACTTGAGCCATTGTGATTGCAACACATAGACAATTGAGCGTCTT 1730  
  
Qy 546 HisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeu 565  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1731 CATCCAAATCCATAAGTTGCTTGTTCCTCATTAACAAGACACTATGTTATAAATGCATCT 1790  
  
Qy 566 AlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrValPheProAlaLys 585  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1791 GCAAGACAAGTTTGTATCAATGCCAATGGCTCTTATCGAAACAACCCCATTCATCAAAA 1850  
  
Qy 586 TyrSerMetGluMetSerAlaValValTyrLysAspTyrValPheProGluGlnAlaLeu 605  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1851 TATTCAATGAGTGTTCATCTATCTTGTAAGGATTGGACCTTCCCTGATCAAGCATTA 1910  
  
Qy 606 ProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSerProLeuGlyIle 625  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1911 CCTAATAATCTCATGAAGAGGACTAGCTGTGGAGGACTCAAGTGCCCCCATGGACTT 1970  
  
Qy 626 ArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTyrSerAlaIle 645  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 1971 AGATTGCTAATAAATGATTATCCATTGCTGTGTGATGCTTTCGACATTGGTCAGCCATT 2030  
  
Qy 646 LysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAlaValGlnLys 665  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2031 AAAACATGGGTACAGGATTATTGTGCTGTCTCTACTACAAGATGACAATGCAGTACAAAAT 2090  
  
Qy 666 AspThrGluLeuGlnAlaTyrTrpLysGluLeuArgGluGluGlyHisGlyAspLysLys 685  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2091 GACTTTGAACCTCCAATCTTGGTGAATGACTAAGAGAGAAAGCCCGCTGACAAGAAA 2150  
  
Qy 686 AspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIle 705  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2151 CATGAACCATGTTGGCCAAAATGCAAACTTAAAGTGAATTAATCGAATCCTGCCTACA 2210  
  
Qy 706 ThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAla 725  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2211 ATTATATGGATTGCTTCAGCTCTTCATGCGCAGTTAACTTTGGACAATATCCCTACGGA 2270  
  
Qy 726 GlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGluProGlySerPro 745  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2271 GGCTATATTCTCAATCGACCAACTACAACTCGTAGGTTTCATGCGCTGAAGTTGGCAGGCT 2330  
  
Qy 746 GlutyrGluGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGln 765  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2331 GAGTACAAAGAACTGGAATCGAATCCGAAAGCTTTCTTGAGAACAAATATGTTTCAGAA 2390  
  
Qy 766 LeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHisSerSerAspThr 785  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2391 TTACAAGCACTTGTAGTATTTCAATTATTGAAATCTTGTCAAAGCATGCTTCTGATGAA 2450  
  
Qy 786 LeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGluProLeuSerAla 805  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2451 GTTTATCTTGGACAAAGAGCTTCAATTGATTGGACTTCAGATAAAATTCATTTGGAAGCA 2510  
  
Qy 806 PheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnVal 825  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2511 TTTGAGAAATTTGGGAAAAAATTTATTGAAGTTGAGAATAGGATCATGGAAAGGAATAAA 2570  
  
Qy 826 AspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThrLeuLeuPhePro 845  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2571 GAGGTGAATTTGAAGAATAGATCTGGACCTGTTAATTTGCCTTATCTACTCTACTTGTCCA 2630  
  
Qy 846 ThrSerGluGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 2631 TCAAGTAACGAAGGACTCACTGGAAGAGGAATTCCTAATAGTATTTCTATC 2681

RESULT 11  
ABX13453  
ID ABX13453 standard; DNA; 2964 BP.  
XX

AC ABX13453;  
XX 04-JUN-2003 (first entry)  
DT  
XX C. sativus lipoxygenase DNA corresponding to Genbank X92890.  
DE  
XX Expression cassette; transgenic; promoter; LOX5; plant; food production;  
KW animal feed; seed; stress resistance; disease resistance; starch content;  
KW lipid content; dormancy; fibre content; pharmaceutical production;  
KW fine chemical production; sterile plant; vitamin; flavouring; perfume;  
KW dye; cotyledon; embryonic tissue; stress factor; LOX; ds.  
XX  
OS Cucumis sativus.  
XX DE10127882-A1.  
PN  
XX 12-DEC-2002.  
PD  
XX 11-JUN-2001; 2001DE-01027882.  
PF  
XX 11-JUN-2001; 2001DE-01027882.  
PR  
XX (BADI ) BASF PLANT SCI GMBH.  
XX  
PI Bischoff F, Feussner I, Loyall LP;  
DR WPI; 2003-279966/28.  
XX  
PT Cassette for expressing transgene, useful e.g. in production of  
PT pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene  
PT of Arabidopsis, provides cotyledon-specific expression.  
XX  
PS Claim 5; Page; 28pp; German.  
XX  
CC This invention describes a novel cassette for the transgenic expression  
CC of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis  
CC thaliana or deletion variants of the LOX5 promoter which are functionally  
CC linked to the nucleic acid of the invention. The cassette is used to  
CC prepare transgenic organisms, especially plants, for production of foods,  
CC animal feeds, seeds (including those with increased resistance to stress  
CC and disease, altered starch/lipid contents or dormancy, or altered fibre  
CC content), pharmaceuticals (especially antibodies, vaccines, enzymes and  
CC pharmaceutical proteins) and fine chemicals (especially enzymes,  
CC vitamins, amino acids, sugars, (un)saturated fatty acids, flavourings,  
CC perfumes and dyes), also to produce sterile plants. The LOX5 promoter  
CC provides strong and specific expression in cotyledons and/or other early  
CC embryonic tissue, so can degrade, or protect against, stress factors to  
CC which these tissues are particularly sensitive. Since cotyledons are the  
CC main storage organs of seeds, expressing transgenes in them produces  
CC targeted increases/modifications in nutritional value. Expression in the  
CC cotyledons is homogeneous, there are no side effects on other plant  
CC organs (pollen) and the promoter is functional in a wide variety of  
CC plants (ornamentals or crops). This sequence represents a nucleic acid  
CC sequence associated with the Arabidopsis thaliana LOX gene described in  
CC the disclosure of the invention  
XX  
SQ Sequence 2964 BP; 988 A; 516 C; 583 G; 877 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2.64e-265 Length: 2964  
Score: 2911.00 Matches: 534  
Percent Similarity: 78.65% Conservative: 140  
Best Local Similarity: 62.31% Mismatches: 175  
Query Match: 64.20% Indels: 8  
DB: Gaps: 6

US-10-731-642A-1 (1-862) x ABX13453 (1-2964)

Qy 6 lleValAspAlaIleThrGlyLysAspAspGlyLysLysValLysGlyThrValValLeu 25  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 135 ATTTTAGATAGAGTTTCCAGTCTT---GGAGGAAACAAATCAAAGGAAAGTGATTCTT 191  
Qy 26 MetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAspGlyValLeu 45

Db 192 ATGAGAACCAATGTTTGGATTCTCACTGAATTTCAATCCAAATCTTCTTGATAACTTCACT 251  
Qy 46 GluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAlaAspProAla 65  
Db 252 GAGCTCTGGGTGGTGGTGTCTTTCCAACTCATTAGTGCCTACTACT-----TCA 305  
Qy 66 AsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeuThrAsnSer 85  
Db 306 AATGACTCAAGAGGAGGAAAGTTGGGAACAAGGCATATTGGAGAGGTGGCTAACTTCAATC 365  
Qy 86 ThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAspAspGluGlu 105  
Db 366 CCACCACCTGTTGCTGGAGAATCAGTGTCCAAATCAACTTTCAATGG--GATGAAAT 422  
Qy 106 PheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhePheLeuLys 125  
Db 423 TTTGGATTCCAGGAGCTTTCTTCATAAAAAATGGACATACAAGTGAATTCTTTCTCAA 482  
Qy 126 SerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCysAsnSerTrp 145  
Db 483 TCTCTCACTTGTGATGATGTTCTCGCTATGGCAGAGTCCATTTTGTGCAATTTCTTGG 542  
Qy 146 ValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGlnAlaTyrLeu 165  
Db 543 GTTTACCCTTCTGGAAGATACAGAAGATCGCATTTTCTTGCCAAATCATGTTTATCTT 602  
Qy 166 ProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValThrLeuArg 185  
Db 603 CCAAGTCAAAACCAACCAACCTCTTCGTAAGTATAGAGAGGAAGAAATGTGGAATTTGAG 662  
Qy 186 GlyAspGlyThrGlyLysLeuGluGluTrpAspArgValTyrAspTyrAlaTyrTyrAsn 205  
Db 663 GGAGATGGAACAGGAGAAAGAAAGGAATGGATAGAAATTTATGACTATGATGTTTATA 722  
Qy 206 AspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSer 225  
Db 723 GACATTGCTGACCCTGATGTTGGTGAT-----CATCGTCCTATTCTCGGTGGACGACC 776  
Qy 226 GluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsn 245  
Db 777 GAATATCCTTACCTCGTAGGGGAAGAACAGGACGACCACGATCAAGAAGAGACCACAAT 836  
Qy 246 SerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArgAspGluArg 265  
Db 837 TATGAGAGCAGATTGTCAACCAATATGAGCTTAGACATCTATGTACCAAAAGATGAAAC 896  
Qy 266 PheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeu 285  
Db 897 TTTGGGCATTTGAAGATGTCAGATTTCTCGTTATACATTAAAGACACTTTCGATATCA 956  
Qy 286 LeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGlu 305  
Db 957 ATCAAACCAGGACTTCAATCCATATTGTGTGTAACCTCCAAATGAATTTGACAATTTTAA 1016  
Qy 306 AspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAla 325  
Db 1017 GAAGTTGATAATCTTTTGAGAGAGGTTTTCCTCCATTCATTTAAT---GCTTTTAAGACC 1073  
Qy 326 IleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGly 345  
Db 1074 CTCACCTGAGGACCTCACTCCACCTTTGTTCAAAGCACTCGTGAGGAATGATGGTGA 1133  
Qy 346 LeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAsp 365  
Db 1134 TTTCTCAAATTTCTTACTCCCGAAGTTGTCAAAGATAATAAAATAGGATGGAGCACTGAT 1193  
Qy 366 GluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGln 385  
Db 1194 GAAGAATTTGCAAGAGAAATGTTAGCAGGACCAATCCTCTATTGATTTCGTCGCTTGA 1253  
Qy 386 GluPheProLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIle 405

Db 1254 GCTTTTCCACCAACAAGTAAGCTTGACCCTCCAAATGTTTATGGGAATCAAAACAGTACCATC 1313  
Qy 406 ThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGluAlaIleLysThr 425  
Db 1314 ACTGAAGAACAACATAAAGCATGGTTTAGATGGTCTTACGGTTGATGAGGCAATGAAGCAA 1373  
Qy 426 AsnArgLeuPheIleLeuAsnHisAspIleLeuMetProTyrLeuArgArgIleAsn 445  
Db 1374 AACAGGCTCTACATAGTGGATTTCATGATGATTAATGCCCTATCTTACAAGGATGAAT 1433  
Qy 446 ThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGly 465  
Db 1434 ---GCAACATCAACAAAAACATATGCCACAAGAACATTGCTTCTTTGAAAGATGATGGG 1490  
Qy 466 ThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheGly 485  
Db 1491 ACTTTGAAGCCATTGGTTATTGAGTTAGCTTGCCACATCTTCAAGGAGATCAACTTGGT 1550  
Qy 486 AlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLeu 505  
Db 1551 GCCATTAGCAAACTATACTTTCCAGCTGAAAATGGAGTTCAAAAATCCATTTGGCAATTG 1610  
Qy 506 AlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeu 525  
Db 1611 GCTAAAGCTTATGTAACCTGTTAATGATGTTGGCTACCATCAACTATTATTAGTCATTGGTTG 1670  
Qy 526 AsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeu 545  
Db 1671 CATACTCATGCTGTACTTGGAGCCATTGTTGATTGCAACACATAGACAATTGAGCGTCTT 1730  
Qy 546 HisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeu 565  
Db 1731 CATCCAATCCATAAGTTGCTTCTCTCATTAACAAGACACTATGTTTATAAATGCATCT 1790  
Qy 566 AlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrValPheProAlaLys 585  
Db 1791 GCAAGACAAGTTTGTATCAATGCCAATGGTCTTATCGAAACAACCCATTATCCATCAAAA 1850  
Qy 586 TyrSerMetGluMetSerAlaValValTyrLysAspTrpValPheProGluGlnAlaLeu 605  
Db 1851 TATTCAATGGAGTTGTCTATCTATCTTGTACAAAGGATTGGACCTTCCCTGATCAAGCATTA 1910  
Qy 606 ProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSerProLeuGlyIle 625  
Db 1911 CCTAATAATCTCATGAAGAGAGGACTAGCTGTGGAGGACTCAAGTGCCCCCATGGACTT 1970  
Qy 626 ArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTrpSerAlaIle 645  
Db 1971 AGATTGCTAATAATGATTATCCATTGCTTGTGTTGATGGTCTTGACATTGTTGGTCCATT 2030  
Qy 646 LysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAspAlaValGlnLys 665  
Db 2031 AAAACATGGGTACAGGATTATTGCTGTCTCTACTACAAAGATGACATGCAAGTACAAAAT 2090  
Qy 666 AspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHisGlyAspLysLys 685  
Db 2091 GACTTTGAACTCCAATCTTGGTGGAAATGAGCTAAAGAGAGAAAGCCCGCTGACAAGAAA 2150  
Qy 686 AspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIle 705  
Db 2151 CATGAACCATGGTGGCCAAAATGCAAACTTTAAGTGAATTAATCGAATCCTGCACTACA 2210  
Qy 706 ThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAla 725  
Db 2211 ATTATATGGATTGCTTCAGCTCTTCATGCCGAGTTAACTTTGGACAATATCCCTACGGA 2270  
Qy 726 GlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGluProGlySerPro 745  
Db 2271 GGCTATATTCTCAATCGACCAACTACAACTCGTAGGTTTCATGCCTGAAGTTGGCACGGCT 2330  
Qy 746 GluTyrGluGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGln 765  
Db 2331 GAGTACAAAGAACTGGAATCGAATCCCGAAAAAGCTTTCTTGAGAACAAATATGTTTCAGAA 2390





Qy 322 LeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSer 341  
Db 952 GCGCTCGAGGACATGGCAAGCTCTTCGGCTCCAGTCGTCAAGGACCTCCTCCCGCC 1011  
Qy 342 AspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAla 361  
Db 1012 GCGGGGACTACCTGCTCAAGCTCCCATCCACAGATCATCCAAGAGGACAAGAACGCG 1071  
Qy 362 TrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIle 381  
Db 1072 TGGAGGACCGACGAGGAGTTCCGCGGAGGTGCTCGCCGGCTCAACCCGATGGTGATC 1131  
Qy 382 SerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGln 401  
Db 1132 ACGCGCTCACGGAGTTCGCCGCCCAAGACACGCTGGACCCCAAGTACGGCACCC 1191  
Qy 402 AsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGlu 421  
Db 1192 ACCAGCACCATCACGGCGGAGCACATCGAGAAGAACCTCGAGGGCTCACGGTGACG 1251  
Qy 422 AlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyrLeu 441  
Db 1252 GCGCTGGACGGCAACAGGCTCTACATCTGGACCAACACGACCGCTTCATGCCGTTCC 1311  
Qy 442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461  
Db 1312 ATCGACGTCAACAACCTGGAGGGCAACTTCATCTACGCCACCAGGACGCTCTTCTTCCTG 1371  
Qy 462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481  
Db 1372 CGCGGGACCGGACGAGCTCGGCCCTCGCATCGAGCTCAGCGAGCGCTACATCGACGG 1431  
Qy 482 AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501  
Db 1432 GACCTCACCTGGCCCAAGCAAGGTCTACACGCCGGCGTCCAGCGGCTCGAGGCCTGG 1491  
Qy 502 IleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle 521  
Db 1492 GTGTGGCAGCTCGCCAAGGCCTATGTGCGCGTCAACGACTCTGGCTGGCACTCGTC 1551  
Qy 522 SerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGln 541  
Db 1552 AGCCACTGGCTGAACACCCACGCGGTGATGGAGCGCTTCGTGATCGCGACGAACCGGCAG 1611  
Qy 542 LeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsn 561  
Db 1612 CTGAGCGTGACGACCCCGGTGCACAAGTCTCCTGAGCTCGCACTTCGCGACACCATGACC 1671  
Qy 562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrVal 581  
Db 1672 ATCAACGCGCTGGCGGGCAGACGCTCATCAACGGCGGCGCATCTTCGAGATGACCGTC 1731  
Qy 582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhePro 601  
Db 1732 TTCCCGGGCAAGTACGCGCTGGGCATGTCTCCGTGGTGTACAAGAGCTGGAATTCACC 1791  
Qy 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSer 621  
Db 1792 GAGCAGGGCCTCCCGCCGACCTCGTCAAGAGGGCGTGGCGGTGGCGGACCCGTCACG 1851  
Qy 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIle 641  
Db 1852 CCGTACAAGGTGCGGCTGCTGATCGAGGACTACCCGTACGCGAGCGACGGCTGGCCATC 1911  
Qy 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAsp 661  
Db 1912 TGGCAGCCCATCGACAGTGGTGGCGGAGTACCTGGCCATCTACTACCCGACGACGGC 1971  
Qy 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHis 681  
Db 1972 GCGCTGCGGGCGGACGAGGAGCTGCAGGCGGTGGTGAAGAGGTGCGCGGAGGTGCGGCAC 2031

Qy 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701  
Db 2032 GCGGACCAAGGACGCGCCTGGTGGCCCAAGATCGAGCGGTGTCGGAGCTCGCCAGC 2091  
Qy 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721  
Db 2092 GCCTGCACCACCATCATCTGGATCGGTTCGGCGCTCCACGCGCGCGTCAACTTCGGCCAG 2151  
Qy 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741  
Db 2152 TACCCGTACGCGGGTACCTCCGAACAGGCCACCGTGAGCCGCGCGGATGCCGGAG 2211  
Qy 742 ProGlySerProGluTyrGluLeuLysThrAsnProAspLysValPheLeuLysThr 761  
Db 2212 CCGGACGAAGGAGTACGAGAGCTGGAGCGGACCCCGAGCGGGCTTCATCCACACC 2271  
Qy 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781  
Db 2272 ATCAGAGCCAGATCCAGACCATCATCGGCATCTCGCTCATCGAGATCCTCTCCAAGCAC 2331  
Qy 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGlu 801  
Db 2332 TCCTCCGACGAGGTGTACCTCGGCCAGCGCGACACCCCGAGTGGACCTCCGACGCCCG 2391  
Qy 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821  
Db 2392 GCGTGGCGGCGTTCAAGAGGTTCAGCGACGCGCTGTTCAAGATCGAGGCAAGTGGTG 2451  
Qy 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841  
Db 2452 GCGGAGAACCGGACCCGACGCTGAGGAACAGGAACGCGCCCGCGAGTCCCTTACATG 2511  
Qy 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855  
Db 2512 CTGCTCTATCCCAACACCTTGACCACAGTGGCGCGCGGAGGGCTCACTGCCAAGGGC 2571  
Qy 856 IleProAsnSerValSerIle 862  
Db 2572 ATCCCAACAGCATCTCCATC 2592  
RESULT 13  
AAD64728  
ID AAD64728 standard; cDNA; 3007 BP.  
XX  
AC AAD64728;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Maize lipoxigenase (CSSAP92) cDNA.  
XX  
KW Maize; lipoxigenase; CSSAP92; aflatoxin; gene therapy; plant protectant;  
KW gene; ss.  
XX  
OS Zea mays.  
XX  
FH Key Location/Qualifiers  
CDS 65..2659  
FT /\*tag= a  
FT /product= "Maize lipoxigenase"  
XX  
PN US6627797-B1.  
XX  
PD 30-SEP-2003.  
XX  
PF 16-MAR-2001; 2001US-00810268.  
XX  
PR 21-MAR-2000; 2000US-0190950P.  
XX  
PA (TEXA ) UNIV TEXAS A & M SYSTEM.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Duwick J, Maddox JR, Keller NP;  
XX

DR WPI; 2003-874315/81.  
DR P-PSDB; ABW02705.  
XX  
PT New maize lipoxigenase polynucleotide, designated CSSAP92, useful for  
PT altering lipoxigenase concentration in plants, for decreasing  
PT accumulation of aflatoxin in plants, or for increasing the resistance of  
PT plants to pathogens.  
XX  
PS Claim 1; SEQ ID NO 1; Opp; English.  
XX  
CC The invention relates to maize lipoxigenase polynucleotide, designated  
CC CSSAP92. The nucleic acid molecule and methods are useful in altering  
CC lipoxigenase concentration in plants, in decreasing accumulation of  
CC aflatoxin in plants, or in increasing the resistance of plants to  
CC pathogens. The invention is useful in gene therapy. The present sequence  
CC is the maize lipoxigenase cDNA  
SQ Sequence 3007 BP; 656 A; 1015 C; 887 G; 449 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 7.96e-253 Length: 3007  
Score: 2779.50 Matches: 525  
Percent Similarity: 74.86% Conservative: 124  
Best Local Similarity: 60.55% Mismatches: 207  
Query Match: 61.30% Indels: 11  
DB: 10 Gaps: 5  
US-10-731-642A-1 (1-862) x AAD64728 (1-3007)  
QY 3 LeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysLysValLysGlyThr 22  
DB 68 CTGAGCGGGATCATCGACGGGCTGACGGGGGGAACAAGCATGCGCGGCTCAAGGGCAG 127  
QY 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42  
DB 128 GTGGTGCTCATGGCAAGAACGTGCTGGACCTCAACGACTTCGGCGGCCACCGTCTGTGAC 187  
QY 43 GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla 62  
DB 188 AGCATCAGCGAGTCTCTCGCAAGGGGTACCTGCCAGTCTCATCAGCTCCACCTCGTC 247  
QY 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82  
DB 248 GACGCCAACACCGCAACCGCGGGGGTTCGGGGCGGAGCGGAACCTGGAGCAGTGGCTG 307  
QY 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102  
DB 308 ACGAGCCTGCCGCTGACGACCGCGGAGTCAAAGTTCGGCGTCACTCGACTGGGAG 367  
QY 103 AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122  
DB 368 GTGGAGAAGCTGGGAGTCCGGGGCGCGTCTGCTCAAGAACAAACACCGCGCGAGTTC 427  
QY 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142  
DB 428 TTCCTCAAGACAATACCCCTCGACGACGTGCCCGCGCGCGCGTCACTTCGTCGCC 487  
QY 143 AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162  
DB 488 AACTCCTGGGTCTACCCCGCGGCAAGTACCGCTACAACCGCGTCTTCTTCCAACGAT 547  
QY 163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182  
DB 548 ACGTACCTGCCAAGCCAGATGCGCGGCGGCTGAAGCCGTACCGCGACGACGAGCTCCGC 607  
QY 183 ThrLeuArgGlyAspGly---ThrGlyLysLeuGluGluTrpAspArgValTyrAspTyr 201  
DB 608 AACCTCCGCGGACGACGACGAGGGCCCTTACGAGGACGACGACCGCGTGTACCGCTAC 667  
QY 202 AlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeu 221  
DB 668 GACGTCTACACGACCTCGCGGAGCCCGACGCGGCGCAAC-----CCGCGCCCATCTCT 721

QY 222 GlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys 241  
DB 722 GCGGGTCCGCGACCAACCCGTACCCGCGCGCTGCCGACGCGGCGCAAGCCACCAAA 781  
QY 242 ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValPro 261  
DB 782 ACCGACCCCAACTCGGATAGCCGACTGCTGCTGGTGGAG-----CAGATCTACGTGCCG 835  
QY 262 ArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSer 281  
DB 836 CGGACGAGCGCTTCGGCCACCTCAAGATGTCCGACTTCTCTGGGTACTCCATCAAGGCC 895  
QY 282 IleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPhe 301  
DB 896 ATCAGCAGGGCATCATCCGCGGGTGGCGACGTACGTGGACACCAACCCGCGGAGTTC 955  
QY 302 AspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGlyPro 321  
DB 956 GACTCCTTCCAGGACATCATCAACCTGTACGAGGGCGGGATCAAGCTGCCCAAGATCCAG 1015  
QY 322 LeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSer 341  
DB 1016 GCGCTCGAGACATGCGCAAGCTCTTCGCGTCCAGCTCGTCAAGGACCTCTCTCCCGCC 1075  
QY 342 AspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAla 361  
DB 1076 GCGGGGACTACCTGCTCAAGCTCCCATCCACAGATCATCCAAAGAGACAAGACGCG 1135  
QY 362 TrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIle 381  
DB 1136 TGGAGGACCGACGAGGAGTTCGCGCGGAGGTGCTCGCGCGCTCAACCGATGGTGATC 1195  
QY 382 SerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGln 401  
DB 1196 ACGCGCTCACGGAGTTCGCGCCCAAGACACGCTGGACCCACGAAAGTACGGCGACAC 1255  
QY 402 AsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGlu 421  
DB 1256 ACCAGCAGATCACGGCGGAGCACATCGAGAAGAACCTCGAGGGCTCAGCGTGCAGCAG 1315  
QY 422 AlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyrLeu 441  
DB 1316 GCGCTGGACGGCAACAGGCTCTACATCTGAGACCAACACGACCGCTTCATCGCTCCTC 1375  
QY 442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461  
DB 1376 ATCAGCTCAACAACCTGGAGGGCAACTTCATCTACGCCACCAAGACGCTCTTCTTCTG 1435  
QY 462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481  
DB 1436 CGCGGCGACGCGAGGCTCGCGCCCTCGCCATCGAGCTCAGCGACGCGTACATCGACGG 1495  
QY 482 AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501  
DB 1496 GACCTCACCGTGGCCAAAGAGCAAGGTCTACACGCGCGCTCCAGCGCGTCCGAGGCTGG 1555  
QY 502 IleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle 521  
DB 1556 GTGTGGCAGCTCGCCAAGGCTATGTGCGCGTCAACGACTCTGGCTGGCACCAACTCGTC 1615  
QY 522 SerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGln 541  
DB 1616 AGCCACTGGCTGAACACCCACGCGGTGATGGAGCCGTTCTGTGATCGGACGAACCGGCG 1675  
QY 542 LeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsn 561  
DB 1676 CTGAGCGTGACGCCCGGTGCACAAGCTCTTGAGCTCGACTTCGCGACACCATGACC 1735  
QY 562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuThrVal 581  
DB 1736 ATCAACGCGCTGGCGGCGAGACGCTCATCAACGCGCGGCGCATCTTTCGAGATGACCGTC 1795  
QY 582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhePro 601

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Db 1796 TTCCCGGCAAGTACGCGTGGCATGTCTCCGTGGTGTAAGAGCTGGAACCTCACC 1855
Qy 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSer 621
Db 1856 GAGCAGGGCTCCCGCCGACCTCGTCAAGAGGGCGTGGCGGTGGCGGACCCGTCCAGC 1915
Qy 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIle 641
Db 1916 CCGTACAGGTGGCGTGTGATCGAGGACTACCCGTACCGGAGGACGGGTGGCCATC 1975
Qy 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrLysSerAspAsp 661
Db 1976 TGGCAGCCATCGAGCAGTGGTGGCGGAGTACCTGGCCATCTACTACCCGACGACGGC 2035
Qy 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGlyHis 681
Db 2036 GCGCTGGGGCGGACGAGGAGCTGCAGCGTGGTGGAGGAGTGGCGGAGTGGGGCAC 2095
Qy 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701
Db 2096 GCGCACCACAAGGACGCGCCCTGGTGGCCCAAGATGCAGGCGGTCTGGAGCTCGCCAGC 2155
Qy 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721
Db 2156 GCCTGCACCAACCATCATCTGGATCGCTCGCGCTCCACGCGCGCTCAACTTCGGCCAG 2215
Qy 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741
Db 2216 TACCCGTACGGGGGTACTCTCCGACAGGCCACCGTGAGCCGCGCGCGGATGCCGGAG 2275
Qy 742 ProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeuLysThr 761
Db 2276 CCGGGCAGCAAGGAGTACGAGGAGCTGGAGCGGACCCGAGGCGCGGCTTCATCCACAC 2335
Qy 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781
Db 2336 ATCAGAGCAGATCCAGACCATCATCGCATCTCGTCTCATCGAGATCCTCTCCAAGCAC 2395
Qy 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGlu 801
Db 2396 TCCTCCGACGAGGTGTACTCTCGGCCAGCGGACACCCCGAGTGGACCTCCGACGCCCGG 2455
Qy 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821
Db 2456 GCGCTGGCGCGCTTCAAGAGGTTTCAGCGACGCGCTGGTCAAGATCGAGGGCAAGGTGTG 2515
Qy 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841
Db 2516 GCGGAGAACCGGACCCGACGCTGAGGACAGGAACGGCCCCCGCGGAGTTCCCTACATG 2575
Qy 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855
Db 2576 CTGCTCTATCCCAACACCTCTGACCACAGTGGCGCGCGCGGAGGGCTCACTGCCAAGGCG 2635
Qy 856 IleProAsnSerValSerIle 862
Db 2636 ATCCCAACAGCATCTCCATC 2656
RESULT 14
ADG93380
ID ADG93380 standard; DNA; 2595 BP.
XX
AC ADG93380;
XX
DT 11-MAR-2004 (first entry)
XX
DE Maize lipoxigenase (LOX) DNA #6.
XX
KW Maize; lipoxigenase; LOX; corn; gene; ds; plant;
KW plant pathogen defence system; plant development; tissue healing;
KW mycotoxin; aflatoxin; sterigmatocystin.
XX
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Zea mays.
XX US2003166855-A1.
PN
XX
PD 04-SEP-2003.
XX
PF 25-APR-2002; 2002US-00132350.
XX
PR 27-APR-2001; 2001US-0286889P.
PR 13-JUL-2001; 2001US-0305366P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Navarro Acevedo PA, Duvick JP, Kolomiets MV, Simmons CR;
XX
DR WPI; 2003-898106/82.
DR P-PSDB; ADG93381.
XX
PT New lipoxigenase polypeptides and polynucleotides, useful for enhancing
PT resistance to pathogens, e.g. fungi, viruses, nematodes or insects, for
PT promoting healing of damage tissues, or for modulating plant growth and
PT development.
XX
PS Disclosure; SEQ ID NO 11; 151pp; English.
XX
CC The invention relates to maize lipoxigenase (LOX) polypeptides and
CC polynucleotides encoding the polypeptides. The LOX polypeptides and
CC polynucleotides are useful in modulating plant pathogen defence systems
CC (particularly enhancing resistance to fungi, viruses, nematodes and
CC insects) and plant development, and for promoting healing of damaged
CC tissues. LOX proteins may also be used to inhibit the production of
CC mycotoxins of fungi (e.g. aflatoxin) and sterigmatocystin producing
CC fungus in plants susceptible to contamination by the mycotoxins. This
CC sequence represents DNA encoding a maize LOX polypeptide of the
CC invention.
XX
SQ Sequence 2595 BP; 505 A; 925 C; 802 G; 363 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.69e-252 Length: 2595
Score: 2769.50 Matches: 524
Percent Similarity: 74.74% Conservative: 124
Best Local Similarity: 60.44% Mismatches: 208
Query Match: 61.08% Indels: 11
DB: 10 Gaps: 5

US-10-731-642A-1 (1-862) x ADG93380 (1-2595)

Qy 3 LeuGlyLysIleValAspAlaIleThrGlyLysAspGlyLysLysValLysGlyThr 22
Db 4 CTGAGCGGGATCATCGACGGGTGACGGGGGCGAACAAGCATCGCGGCTCAAGGGCACG 63
Qy 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42
Db 64 GTGTGTCTCATGCGCAAGAACGTGTGGACCTCAACGACTTCGGCGCCACCGTCGTTGAC 123
Qy 43 GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla 62
Db 124 AGCATCAGCGAGTTCTCTCGGCACAGGGGTTCACCTGCCAGTTCATCAGCTCCACCCTCGTC 183
Qy 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82
Db 184 GACGCCAACACGGCAACCCGCGGGCGGTTCGGGGCGGAGGCGCAACCTGGAGCAGTGGCTG 243
Qy 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
Db 244 ACGAGCTGCCGTCTGTCAGCACCGCGGAGTCCAAGTTCGGCGTCACGTTTCGACTGGGAG 303
Qy 103 AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122
Db 304 GTGGAGAAGTGGGAGTGCCTGGGGGCGCGTTCGTCTGTCGAAGAACAACACCGCCGAGTTC 363
Qy 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
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Db 364 TTCCTCAAGACATACCTCGACGACGTGCCCGCGCGCGCTTCCTTCGTCGCC 423  
QY 143 AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162  
Db 424 AACTCCTGGGTCTACCCCGCGGCAAGTACCGCTACAACCGCGTCTTCTTCCAAAGAT 483  
QY 163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182  
Db 484 ACGTACCTGCCAAGCCAGATGCCGGCGGCTGAAGCCGTACCGGACGACGAGCTCCGC 543  
QY 183 ThrLeuArgGlyAspGly--ThrGlyLysLeuGluGluTrpAspArgValTyrAspTyr 201  
Db 544 AACCTCCGGCGGACGACCAAGAGGGCCCTTACAGGAGCAGCACCGCGTGTACCGGTAC 603  
QY 202 AlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeu 221  
Db 604 GACGTCTACAACGACCTCGCGGAGCCCGACGGGGCAAC-----CCGCGCCCCATCCTC 657  
QY 222 GlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys 241  
Db 658 GCGGCTCCGCGCACCAACCGTATCCCGCGCGCTGCCGACGCGGCGCAAGCCCAAAA 717  
QY 242 ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValPro 261  
Db 718 ACCGACCCCAACTCGGATAGCCGACTGTCTCGTGGTGGAG-----CAGATCTACGTGCCG 771  
QY 262 ArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSer 281  
Db 772 CGGGACGAGCGCTTCGGCCACCCTCAAGATGTCCGACTTCTTGGGTACTCTCCATCAAGGCC 831  
QY 282 IleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPhe 301  
Db 832 ATCACGCGAGGCGCATATCCCGCGGTGCGCACGTACGTGGACACCAACCCCGGCGAGTTC 891  
QY 302 AspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGlyPro 321  
Db 892 GACTCCTTCAGGACATCATCAACCTGTACGAGGGCGGGATCAAGTGCCCAAGATCCAG 951  
QY 322 LeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSer 341  
Db 952 GCGCTCGAGGACATGCGCAAGCTCTTCCCGCTCCAGCTCGTCAAGACCTCTCTCCCGCC 1011  
QY 342 AspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAla 361  
Db 1012 GCGGGGACTACCTGTCTCAAGCTCCCATCCACAGATCATCCAAGAGGACAAGAACGCG 1071  
QY 362 TrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIle 381  
Db 1072 TGGAGGACGACGAGGAGTTTCGCGGGGAGGTGCTCGCCGCGCTCAACCCGATGGTGATC 1131  
QY 382 SerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGln 401  
Db 1132 ACGCGCTCACGGAGTTCCCGCCCCAAGACGCTGGACCCCAAGTACGGCGACCCAC 1191  
QY 402 AsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGlu 421  
Db 1192 ACCAGCAGATCACGGCGGAGCACATCGAGAAGAACCTCGAGGGCCTCACGGTGCAGCAG 1251  
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QY 442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461  
Db 1312 ATCGAGTCAACAACCTGGAGGGTAACCTTCATCTACGCCACCAAGACCTCTTCTTCTCTG 1371  
QY 462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481  
Db 1372 CGCGGCGACGGCAGGCTCGCGCCCTCGCTATCGAGCTCAGCGAGCCGTATCAGCAGCGG 1431  
QY 482 AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501  
Db 501

Db 1432 GACCTTACCGTGGCCAAAGAGCAAGGTCTTACACGCGCGGTCTACAGCGCGTTCGAGGCTGG 1491  
QY 502 IleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle 521  
Db 1492 GTGTGGCAGCTCGCCAAGGCTTATGTCCCGTCAACGACTCTGGCTGGCACCAACTCGTC 1551  
QY 522 SerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGln 541  
Db 1552 AGCCACTGGCTGAACACGACGCGCGGTGATGGAGCCGTTCTGTGATCGGACGAACCGGCG 1611  
QY 542 LeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsn 561  
Db 1612 CTGAGCGTGACGCACCCGGTGCACAAGCTCCTGAGCTCGACTTCCGCGACCATGACC 1671  
QY 562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrVal 581  
Db 1672 ATCAACGCGTGGCGGCGAGACGCTCATCAACGCGCGGCGCATCTTCGAGATGACCGTC 1731  
QY 582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhePro 601  
Db 1732 TTCCCGGGCAAGTACGCGTGGGCATGTCTCCGTGGTGTACAAGAGCTGGAACCTTCACC 1791  
QY 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSer 621  
Db 1792 GAGCAGGCGCTCCCCCGCCGACCTCGTCAAGAGGGCGTGGCGGTGGCGGACCCGTCCAGC 1851  
QY 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIle 641  
Db 1852 CTGTACAAGGTGCGGTGCTGATCGAGGACTACCCGTACGCGAGCGACGGGTGGCCATC 1911  
QY 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAsp 661  
Db 1912 TGGACGCCCATCGAGCAGTGGGTGGGCGAGTACCTGGCCATCTACTACCCCGACGCGC 1971  
QY 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGlyHis 681  
Db 1972 GCGCTCGGGGCGACGAGGAGCTGCAGGCGTGGTGAAGGAGTGCAGGAGTTCGGGCAC 2031  
QY 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701  
Db 2032 GCGGACCAAGGACGCGCCCTGTGGCCCCAAGATGCAGGCGCGTGTTCGGAGCTCGCCAGC 2091  
QY 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721  
Db 2092 GCCTGCACCAACCATCATCTGGATCGGTTCGGCGCTCCACGCGCGCTCAACTTCGGCCAG 2151  
QY 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741  
Db 2152 TACCGGTACGGGGGTACCTCCGAACAGGCCCCACGGTGAGCGCGCGCGGATGCCGGAG 2211  
QY 742 ProGlySerProGluTyrGluLeuLysThrAsnProAspLysValPheLeuLysThr 761  
Db 2212 CCGGCGAGCAAGGAGTACGAGAGCTGGAGCGCGACCCCGAGCGCGGCTTCATCCACACC 2271  
QY 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781  
Db 2272 ATCAGAGCCAGATCCAGACCATCATCGGCATCTCGCTCATCGAGATCCTCTCCAAGCAC 2331  
QY 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGlu 801  
Db 2332 TCCTCCGACGAGGTGTACCTCGGCCAGCGGACACCCCGAGTGGACCTCCGACGCCCGG 2391  
QY 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821  
Db 2392 GCGTGGCGGCGTTCAAGAGGTTCAGCGACGCGCTGGTCAAGATCGAGGGCAAGGTGGTG 2451  
QY 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841  
Db 2452 GSCGAGAACCGGACCCCGCAGCTGAGGAACAGGAACGCGCCCGCGAGTTCCTCCCTACATG 2511  
QY 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855  
Db 2512 CTGCTCTACCCCAACACCTCTGACCAAGTGGCGCGCGCGCAGGGGCTCACTGCCAAGGSC 2571

QY 856 IleProAsnSerValSerIle 862  
|||||  
Db 2572 ATCCCCAACAGCATCTCCATC 2592

RESULT 15  
ADG93378  
ID ADG93378 standard; DNA; 3007 BP.

XX AC ADG93378;

XX 11-MAR-2004 (first entry)

DE Maize lipoxygenase (LOX) DNA #5.

XX Maize; lipoxygenase; LOX; corn; gene; ds; plant;  
KW plant pathogen defence system; plant development; tissue healing;  
KW mycotoxin; aflatoxin; sterigmatocystin.

XX Zea mays.

OS US2003166855-A1.

PN 04-SEP-2003.

XX 25-APR-2002; 2002US-00132350.

XX 27-APR-2001; 2001US-0286889P.

PR 13-JUL-2001; 2001US-0305366P.

XX (PION-) PIONEER HI-BRED INT INC.

PA Navarro Acevedo PA, Duvick JP, Koloniets MV, Simmons CR;

PI WPI; 2003-898106/82.

XX P-PSDB; ADG93379.

PT New lipoxygenase polypeptides and polynucleotides, useful for enhancing  
PT resistance to pathogens, e.g. fungi, viruses, nematodes or insects, for  
PT promoting healing of damage tissues, or for modulating plant growth and  
PT development.

XX Disclosure; SEQ ID NO 9; 151pp; English.

CC The invention relates to maize lipoxygenase (LOX) polypeptides and  
CC polynucleotides encoding the polypeptides. The LOX polypeptides and  
CC polynucleotides are useful in modulating plant pathogen defence systems  
CC (particularly enhancing resistance to fungi, viruses, nematodes and  
CC insects) and plant development, and for promoting healing of damaged  
CC tissues. LOX proteins may also be used to inhibit the production of  
CC mycotoxins of fungi (e.g. aflatoxin) and sterigmatocystin producing  
CC fungus in plants susceptible to contamination by the mycotoxins. This  
CC sequence represents DNA encoding a maize LOX polypeptide of the  
CC invention.

XX Sequence 3007 BP; 656 A; 1012 C; 887 G; 452 T; 0 U; 0 Other;

Alignment Scores:  
Pred. NO.: 7.07e-252 Length: 3007  
Score: 2769.50 Matches: 524  
Percent Similarity: 74.74% Conservative: 124  
Best Local Similarity: 60.44% Mismatches: 208  
Query Match: 61.08% Indels: 11  
DB: 10 Gaps: 5

US-10-731-642A-1 (1-862) x ADG93378 (1-3007)

QY 3 LeuGluLysIleValAspAlaIleThrGlyLysAspAspGlyLysLysValLysGlyThr 22  
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Db 68 CTGACGGGATCATCGCGGCTGACGGGGCGGACAGCATCGCGGCTCAAGGCACG 127  
|||  
QY 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42  
|||||

Db 128 GTGTGTCTATGCGCAAGAACGTGTGGACCTCAACGACTTCGGCGCCACCGTTCGTTGAC 187  
QY 43 GlyValLeuGluPheLeuGlyArgValSerLeuGluLeuLeuSerSerValAsnAla 62  
::: |||||  
Db 188 AGCATCAGCGAGTTCTCTCGCAAGGGGTACCTGCCAGTTCATCAGTCCACCCTCGTC 247  
63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82  
||| ||||| ::|||  
Db 248 GACGCCAACACGGCAACCGCGGGGTGCGGGCGGAGGAGAACCTGGAGCAGTGGCTG 307  
83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102  
|||::: |||||  
Db 308 ACGAGCCTGCCGTGCTGACGACCGCGGAGTCCAAGTTCGGCGTCACGTTCCGACTGGGAG 367  
103 AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122  
|||::: |||||  
Db 368 GTGAGAAAGCTGGAGTCCGGGGCGCTGCTCGTCAAGAACCAACACGCGCGGAGTTC 427  
123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142  
||| |||||  
Db 428 TTCCTCAAGACAATCACCCCTCGACGACGTGCCCGCGCGCGCTCACCTTCGTCGCC 487  
143 AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162  
||| |||||  
Db 488 AACTCTCTGGGTCTACCCCGCGGCAAGTACCGCTACAACCGCTCTTCTTCTCCAACGAT 547  
163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluVal 182  
||| |||||  
Db 548 ACGTACTGCCAAGCCAGATCCCGCGGCGCTGAAGCCGTACCGGACGACGAGTCCGC 607  
183 ThrLeuArgGlyAspGly---ThrGlyLysLeuGluGluTrpAspArgValTyrAspTyr 201  
||| |||||  
Db 608 AACCTCCGCGCGACGACGACGAGGAGGCGCCCTACCAGGAGCAGACCGGTGTACCGGTAC 667  
202 AlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeu 221  
||| |||||  
Db 668 GACGTCTACAACGACCTCGGCGAGCGCGACGCGGCAAC-----CCGCGCCCCATCCTC 721  
222 GlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys 241  
||| |||||  
Db 722 GCGGCTCCGCGACCAACCCGTACCCCGCGCTGCCGCGCTGCCGACGCGGCGAAGCCACCAA 781  
242 ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValPro 261  
||| |||||  
Db 782 ACCGACCCCAACTCGGATAGCCGACTGTGCTGGTGAG-----CAGATCTACGTGCCG 835  
262 ArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSer 281  
||| |||||  
Db 836 CGGGACGAGCGCTTCGGCCACCTCAAGATGTCGACTTCTCTGGGCTACTCCATCAAGGCC 895  
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||| |||||  
Db 896 ATCAGCAGGGCATCATCCCGCGGTGCGCACGTACGTGGACACCAACCCCGCGGAGTTC 955  
302 AspSerPheGluAspValLeuLysLeuTyrGluGlyIleLysLeuProGlnGlyPro 321  
||| |||||  
Db 956 GACTCTTCCAGGACATCATCAACCTGTACGAGGCGGGATCAAGTGCCTCAAGATCCAG 1015  
322 LeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSer 341  
|||::: ::|||  
Db 1016 GCGCTCGAGGACATGCGAAGCTCTTCCCGCTCCAGTTCGTCAAGGACCTCTCCCGGCC 1075  
342 AspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAla 361  
|||::: |||||  
Db 1076 GCGGGGACTACCTGCTCAAGCTCCCCCATCCACAGATCATCCAAGAGGACAAGACGCG 1135  
362 TrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIle 381  
||| |||||  
Db 1136 TGGAGGACCGACGAGGAGTTCCGCGGGGAGGTGCTCGCGGCTCAACCCGATGGTGATC 1195  
382 SerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGln 401  
::: |||||  
Db 1196 ACGCGCCTCACGAGTTCCCGCCCAAGAGCAGCGCTGGACCCCAAGCAAGTACGCGGACAC 1255

QY 402 AsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGlu 421  
Db 1256 ACCAGCAGATCACGGCGGAGCACATCGAGAGAAGAACCTCGAGGGCCTCACGGTGCAGCAG 1315  
QY 422 AlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyrLeu 441  
Db 1316 GCGCTGGACGGCAACAGGCTCTACATCTGTGACCACACGACCGCTTCATGCGGTTCCCTC 1375  
QY 442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461  
Db 1376 ATCGACGTCAACAACTGGAGGGTAACCTTCACTACGCCACACGAGACCTCTTCTTCCTG 1435  
QY 462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481  
Db 1436 CGCGGCGACGGCAGGCTCGGCCCTCGCTATCGAGCTCAGCGAGCCGTACATCGACGGG 1495  
QY 482 AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501  
Db 1496 GACCTTACCGTGGCCAAAGAGCAAGGTCTACACGCCGGCGTCCAGCGCGCTCGAGGCCTGG 1555  
QY 502 IleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle 521  
Db 1556 GTGTGGCAGCTCGCCAAAGGCCTATGTGCGCCGCTCAACGACTCTGGCTGGCAACAACTCGTC 1615  
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QY 542 LeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsn 561  
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QY 562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrVal 581  
Db 1736 ATCAACGCGCTGGCGCGGAGACGCTCATCAACGGCGGCGGCATCTTCGAGATGACCGTC 1795  
QY 582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhePro 601  
Db 1796 TTCCCGGGCAAGTACGCGCTGGGCATGTCTCTCGTGGTGTACAAGAGCTGGAACTTCACC 1855  
QY 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSer 621  
Db 1856 GAGCAGGGCCTCCCGCCGACCTCGTCAAGAGGGCGGTGGCGGTGGCGGACCCGTCCAGC 1915  
QY 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIle 641  
Db 1916 CTGTACAAGGTGGGCTGTGATCGAGGACTACCCGTACGCGAGCGACGGGCTGGCCATC 1975  
QY 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAsp 661  
Db 1976 TGGCAGCCCATCGACGAGTGGGTGGCGAGTACTTGGCCATCTACTACCCCGACGACGGC 2035  
QY 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHis 681  
Db 2036 GCGCTGCGGGGCGACGAGGAGCTGCAGGCGTGGTGAAGGAGGTGCGCGAGGTGCGGCAC 2095  
QY 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701  
Db 2096 GCGGACCACAAGACCGCCCTTGGTGGCCCAAGATGACGGCCGTGTGCGAGCTCGCCAGC 2155  
QY 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721  
Db 2156 GCCTGCACCACCATCATCTGGATCGCTCGGCGGTCCACGCCCGCTCAACTTCGGCCAG 2215  
QY 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741  
Db 2216 TACCCGTACGCGGGGTACCTCCGGAACAGGCCCGCGGTGAGCCGCGCGCGATGCCGGAG 2275  
QY 742 ProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeuLysThr 761  
Db 2276 CCCGGCAGCAAGGAGTACGAGGAGCTGGAGCGCGCACCCGCGGCGGTTCATCCACACC 2335

QY 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781  
Db 2336 ATCAGGAGCCAGATCCAGACCATCATCGGCATCTCGTCTCATCGAGATCCTCTCCAAGCAC 2395  
QY 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThrLysAspGlnGlu 801  
Db 2396 TCCTCCGACGAGGTGTACCTCGGCCAGCGGACACACCCCGAGTGGACCTCCGACGCCCGG 2455  
QY 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821  
Db 2456 GCGCTGGCGCGGTTCAAGAGGTTTCAGCGACCGGCTGGTCAAGATCGAGGCAAGGTGGTG 2515  
QY 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841  
Db 2516 GCGGAGAACCCGACCCGACCTCTGAGCAACAGGAACGCGCCCGCGAGTTCCTTACATG 2575  
QY 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855  
Db 2576 CTGCTCTACCCCAACACCTCTGACCACAGTGGCGCGCGCGAGGGGTCACTGCCAAGGGC 2635  
QY 856 IleProAsnSerValSerIle 862  
Db 2636 ATCCCCAACAGCATCTCCATC 2656

Search completed: March 14, 2005, 06:02:38  
Job time : 1196 secs





GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 14, 2005, 04:51:55 ; Search time 352 Seconds  
(without alignments)  
4007.019 Million cell updates/sec

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Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues  
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3625.5	80.0	2871	3	US-09-051-465-2
2	3625.5	80.0	2871	3	US-09-051-465-4
3	3463.5	76.4	2441	3	US-09-051-465-1
4	3254.5	71.8	4237	4	US-09-978-522-4
5	3138	69.2	4687	4	US-09-978-522-2
6	2779.5	61.3	2595	4	US-09-810-268-2
7	2779.5	61.3	3007	4	US-09-810-268-1
8	2680	59.1	2818	4	US-09-751-687-10
9	2280.5	50.3	4663	4	US-09-751-687-8
10	2273.5	50.1	4663	4	US-09-751-687-11
11	1746.5	38.5	2945	4	US-09-714-767A-3
12	1710	37.7	1196	4	US-09-978-522-23

c	13	647.5	14.3	636	4	US-09-978-522-12	Sequence 12, Appl
	14	559.5	12.3	2028	4	US-09-902-540-5455	Sequence 5455, Ap
	15	559.5	12.3	41310	4	US-09-902-540-1264	Sequence 1264, Ap
	16	546	12.0	2496	4	US-09-949-016-5821	Sequence 5821, Ap
	17	546	12.0	2497	4	US-09-023-655-1155	Sequence 1155, Ap
	18	546	12.0	2497	4	US-10-071-411A-3	Sequence 3, Appli
	19	546	12.0	2497	4	US-09-949-016-109	Sequence 109, App
	20	537.5	11.9	3205	3	US-09-061-768A-3	Sequence 3, Appli
	21	537.5	11.9	3205	4	US-09-764-246-3	Sequence 3, Appli
	22	537	11.8	2307	4	US-09-799-451-803	Sequence 803, App
	23	537	11.8	2604	4	US-09-547-435-23	Sequence 23, Appl
	24	537	11.8	2701	4	US-09-547-435-1	Sequence 1, Appli
	25	537	11.8	3384	4	US-09-547-435-29	Sequence 29, Appl
	26	527	11.6	2236	4	US-09-547-435-5	Sequence 5, Appli
	27	511.5	11.3	2469	3	US-09-087-727-1	Sequence 1, Appli
	28	511.5	11.3	2469	4	US-09-853-053-1	Sequence 1, Appli
	29	511.5	11.3	2469	4	US-09-949-016-155	Sequence 155, App
	30	496	10.9	2674	4	US-09-949-016-3041	Sequence 3041, Ap
	31	496	10.9	2685	3	US-09-061-768A-1	Sequence 1, Appli
	32	496	10.9	2685	4	US-09-764-246-1	Sequence 1, Appli
	33	496	10.9	2685	4	US-09-949-016-156	Sequence 156, App
	34	469.5	10.4	2343	3	US-09-641-638-652	Sequence 652, App
	35	469.5	10.4	2343	4	US-10-170-097-652	Sequence 652, App
	36	450.5	9.9	1848	4	US-09-547-435-9	Sequence 9, Appli
	37	450.5	9.9	2316	4	US-09-547-435-27	Sequence 27, Appl
	38	440.5	9.7	1383	4	US-09-547-435-11	Sequence 11, Appl
	39	414.5	9.1	2079	4	US-09-252-991A-3097	Sequence 3097, Ap
	40	390	8.6	1441	4	US-09-547-435-13	Sequence 13, Appl
	41	319.5	7.0	639	4	US-09-978-522-11	Sequence 11, Appl
	42	303.5	6.7	588	4	US-09-547-435-19	Sequence 19, Appl
	43	300	6.6	340	1	US-08-181-271A-40	Sequence 40, Appl
	44	300	6.6	340	1	US-08-449-315-40	Sequence 40, Appl
	45	300	6.6	340	1	US-08-444-803-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1  
US-09-051-465-2  
; Sequence 2, Application US/09051465A  
; Patent No. 6355862  
; GENERAL INFORMATION:  
; APPLICANT: Handa, Avtar K.  
; APPLICANT: Kausch, Kurt D.  
; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting  
; TITLE OF INVENTION: Production of Lipoxigenase in Fruits  
; FILE REFERENCE: 7024-297  
; CURRENT APPLICATION NUMBER: US/09/051.465A  
; CURRENT FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: PCT/US96/16387  
; PRIOR FILING DATE: 1996-10-11  
; PRIOR APPLICATION NUMBER: 60/005,404  
; PRIOR FILING DATE: 1995-10-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: ASCII  
; SEQ ID NO 2  
; LENGTH: 2871  
; TYPE: DNA  
; ORGANISM: Lycopersicon esculentum  
US-09-051-465-2

Alignment Scores:			
Pred. No.:	0	Length:	2871
Score:	3625.50	Matches:	685
Percent Similarity:	87.49%	Conservative:	70
Best Local Similarity:	79.37%	Mismatches:	103
Query Match:	79.96%	Indels:	5
DB:	3	Gaps:	3
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QY	1	MetPheLeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysVallys	20

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Qy 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40

Db 105 GGAAGAGTGATTTTGATGAAAAAATGTTCTAGACTTCATTAATATAGGTGCTTCAGTT 164

Qy 41 LeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSer---Ser 59

Db 165 GTTGATGGCAATTTCTGATTTACTTGGCCAAAAAGTCTCTATCCAAATTGATAAGTGGTTCT 224

Qy 60 ValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGlu 79

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Db 276 AGTTGGCTTACAGACATCACCCCAATAACAGCAGGGGAATCAACTTTTAGTGTACATTT 335

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Qy 220 ValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysPro 239

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Qy 580 ThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpVal 599

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Db 1833 TTCCCTGAACAAGCACTTCCTGCTGATCTCCTCAAAAGAGAGAGTGCTGTTGAGGACTTG 1892

Qy 620 SerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeu 639

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Qy 700 IleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPhe 719

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; Sequence 1, Application US/09051465A  
; Patent No. 6355862  
; GENERAL INFORMATION:  
; APPLICANT: Handa, Avatar K.  
; APPLICANT: Kausch, Kurt D.  
; TITLE OF INVENTION: Improvement of Fruit Quality by Inhibiting  
; TITLE OF INVENTION: Production of Lipoxigenase in Fruits  
; FILE REFERENCE: 7024-297  
; CURRENT APPLICATION NUMBER: US/09/051,465A  
; CURRENT FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: PCT/US96/16387  
; PRIOR FILING DATE: 1996-10-11  
; PRIOR APPLICATION NUMBER: 60/005,404  
; PRIOR FILING DATE: 1995-10-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: ASCII  
; SEQ ID NO 1  
; LENGTH: 2441  
; TYPE: DNA  
; ORGANISM: Lycopersicon esculentum  
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Score: 3463.50 Matches: 650  
Percent Similarity: 87.88% Conservative: 68  
Best Local Similarity: 79.56% Mismatches: 94  
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DB: 3 Gaps: 3  
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QY 59 ---SerValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaIleTyr 77  
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QY 78 LeuGluAsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgVal 97  
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QY 98 ThrPheAspTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeu 117  
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QY 158 PhePheAlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArg 177  
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Db 1373 GTTGAAGGTTCTATCTGGCAGTTTGC AAAAGCCTATGTAGCAGTGAATGACATGGGCATT 1432  
QY 518 HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAla 537  
Db 1433 CATCAGCTCATTAGCCACTGGTTGAATACACACGCGGTGATCGAACCATTTGTGATTGCA 1492  
QY 538 ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg 557  
Db 1493 ACAAAATAGGCATCTAAGTGTGCTTTCATCCCATTTCAATAAATCTTCTCATCCTCATTTCCGT 1552  
QY 558 GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeu 577  
Db 1553 AACACGATGAACATAAATGCTTTAGCAAGAGAGACCTTGACCTATGATGGTGGT---TTT 1609  
QY 578 GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp 597  
Db 1610 GAGACGTCTCTTTTCTCTGCCAAATATTCATGGAAATGTCAGCAGCAGCTTACAAAGAT 1669  
QY 598 TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGlu 617  
Db 1670 TGGGTTTTCCTGAACAAGCACTTCCTGCTGATCTCCTCAAAGAGGAGTGGCTGTTGAG 1729  
QY 618 AspSerSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAsp 637  
Db 1730 GACTTGAGCTCCCAACATGGCATTTCGTTACTGATTCTGGACTATCCATATGCTGTTGAT 1789  
QY 638 GlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyr 657  
Db 1790 GGCTTGGAAATTTGGGCAGCAATCAAAAAGTTGGGTAAACAGAAATATTGCAAGTTCTATTAC 1849  
QY 658 LysSerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArg 677  
Db 1850 AAATCTGACGAGACAGTAGAGAAAGACACTGAACCTCCAAGCTTGGTGGCTAAACTGCAAACTCGACAA 1909  
QY 678 GluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGln 697  
Db 1910 GAAGAGGACATGGCGACAAGAAAGATGAGGCTTGGTGGCTTAACTGCAAACTCGACAA 1969  
QY 698 GluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaVal 717  
Db 1970 GAGCTCAGAGATTGTTGCACCATCATATATATGATAGTAGCTTCAGCACTTCATGCAGCACTC 2029  
QY 718 AsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsn 737  
Db 2030 CATTTTGGCTTATACTCTTACGCTGGTTATCTCCCTAATCGCCCTACTTTAAGCTGTAAT 2089  
QY 738 PheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysVal 757  
Db 2090 TTGATGCCAGAGCCAGGAAGTGTGAGTATGAAGAGCTCAAGACAAATCCAGACAAGGTA 2149  
QY 758 PheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIle 777  
Db 2150 TTCTCTAAAAACATTTGTTCTCTCAGTTGCAATCACTGCTTGAATTTCCATCTTTGAGGTC 2209  
QY 778 LeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThr 797  
Db 2210 TCGTCAAGGCATGCTTCAGATGAGGTTTACTTTGGGACAAAGGGACTCAATTGAATGGACA 2269  
QY 798 LysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGlu 817  
Db 2270 AAGGATAAAGAAACCACTTGTAGCTTTTGAGAGGTTTGGAAAGATGCTTAAGTGATATCGAG 2329  
QY 818 AspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLys 837  
Db 2330 AATCGAATTATGATAATGAATAGTATCAAGAGTTTGGAAAGAACAGGTCAGGGCCTGTTAAC 2389  
QY 838 ValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLys 854  
Db 2390 GTTCCATATACGTTGCTCTTTTCCCAAGTGAAGAGGGACTCACAGGCAAA 2440  
RESULT 4  
US-09-978-522-4



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; Sequence 4, Application US/09978522
; Patent No. 6787684
; GENERAL INFORMATION:
; APPLICANT: Descenzo, Richard
; APPLICANT: Irelan, Nancy
; TITLE OF INVENTION: Lipoxxygenase Genes From Vitis Vinifera
; FILE REFERENCE: 29520/37890
; CURRENT APPLICATION NUMBER: US/09/978,522
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,220
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 4237
; TYPE: DNA
; ORGANISM: Vitis LOX sequence 2
US-09-978-522-4

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Alignment Scores:		
Pred. No.:	0	4237
Score:	3254.50	660
Percent Similarity:	63.28%	105
Best Local Similarity:	54.59%	93
Query Match:	71.78%	355
DB:	4	10
		Length:
		Matches:
		Conservative:
		Mismatches:
		Indels:
		Gaps:

US-10-731-642A-1 (1-862) x US-09-978-522-4 (1-4237)

QY	3	LeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysValLysGlyThr	22
Db	4	ATTCAATTCATTGTGGTGCCATTACTGGCGAAATGATAAGAAGATCAAGGAAC	63
QY	23	ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp	42
Db	64	GTTGTGTTGATGAAGAAGAAATGTTGGATTTTAATGACTTCAATGCATCGGTTCTGGAC	123
QY	43	GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla	62
Db	124	CGGGTTTCATGAGCTGTTGGGACAGGGAGTCCCTCTGCAGCTCGTCAGTGTGTTCA	183
QY	63	AspPro-----	64
Db	184	GATCCTGGTGAGTTTTTTAATTTAATTTAATTTTATTTTTTTCATGTTTTTGTATGAT	243
QY	64	-----	64
Db	244	GGGGTTATTGAAGTTGGGGAGAGGAGAATGATGCCGTTTTTGTGAGGGGTGAGATGGGTT	303
QY	64	-----	64
Db	304	TTGAGTTTTTGATGATGGGAGTTGGAGAAGATGTGTTTTTTTGGAAAGGTCAGAGGGGT	363
QY	64	-----	64
Db	364	TATTCTCAGAAAATTGAGTCAATGAGTTCTTTGACATCTTCCAATTCACCTGGGCAC	423
QY	65	-----	67
Db	424	TAAAGTGCTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTAGCAAATGGG	483
QY	68	LeuGlnGlyLysArgSerLysAlaAlaTyrlLeuGluAsnTrpLeuThrAsnSerThrPro	87
Db	484	TTACAGGGGAAAAATTGGAACCAGCATACTTGGAAAGACTGGATTACCCACAATAACTCT	543
QY	88	IleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAspGluGluPheGly	107
Db	544	TTAACCGCGGGCGAGTCTGCATTCAAGGTCACGTTCCGACTGG--GATGAGGAGATTGGA	600
QY	108	ValProGlyAlaPheIlelleLysAsnLeuHisPheSerGluPhePheLeuLysSerLeu	127
Db	601	GAGCCAGGGGCATTCAATAATTAGAAACAATCACCAAGTGTGTTTTTACCTCAGGACTCTC	660

QY	128	ThrLeuGluAspValProAsnHisGlyLysValHisPheValCysAsnSerTyrValTyr	147
DB	661	ACTCTTGAAGATGTTCTTGACGTGGCAGAAATTCACCTTTGTTTGTAAATTCCTGGGTCTAC	720
QY	148	ProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsn-----	161
DB	721	CCTGCTCAGCACACAAAACTGACCGTGTCTTCTTCACTAATCAGGTAAGACATAATTTAC	780
QY	161	-----	161
DB	781	TTGATACTAGGAGAGTCTGCTGTGGCATTTGTGGCTCATTTGAGCTTAGGCAAGGAGAATTG	840
QY	162	-----GlnAlaTyrLeuProSerGluThrPro	170
DB	841	TCTGCTAAAGGAATGTGTTTATTTATCTGCTGCAGACATATCTTCCAAGTGAAACACCA	900
QY	171	AspThrLeuArgLysTyrArgGluAsnGluLeuValThrLeuArgGlyAspGlyThrGly	190
DB	901	GGGCCACTGCGCAAGTACAGAGAAAGGGGAATGGTGAATCTGAGGGAGATGGAACCGGA	960
QY	191	LysLeuGluGluTyrAspArgValTyrAspTyrAlaTyrTyrAsnAspLeuGlyAspPro	210
DB	961	GAGCTTAAGGAATGGGATCGAGTGTATGACTATGCTTACTATAATGATTTGGGAATCCA	1020
QY	211	AspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSerGluTyrProTyrPro	230
DB	1021	GACAGGGATCTCAAATACGCCCGCCCTGTGCTGGGAGGATCTGCAGAGTATCCTTATCCC	1080
QY	231	ArgArgGlyArgThrGlyArgLysProThr-Lys-----	241
DB	1081	AGGAGGGGAAGAACTGGTAGACCCACCATCTGAAAAAGGTAGATATTGATGCAAAAATTC	1140
QY	241	-----	241
DB	1141	ATATTGTTTCTCATGCTTTTATCATAAAGGATGAATATGATTGATTCTGCTCTTCTT	1200
QY	242	-----ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyr	259
DB	1201	TTAATTAACAGATCCCAACACCGAGAGCAGATTGCCACTTGTGATGAGCTTAAACATATA	1260
QY	259	rValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLe	279
DB	1261	TGTTCCACAGATGAAAGATTGGTCACCTGAAGATGTCAGACTTCTCTGGCTTATGCCCT	1320
QY	279	uLysSerIleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAs	299
DB	1321	GAAATCCATAGTTCAATTCTCTTCTCCCTGAGTTGAGGCTCTATGTGACATCACCCACAA	1380
QY	299	nGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlu	319
DB	1381	TGAGTTTGACAGCTTCCAAGATGTATTAGACCTCTACGAAGGAGGAATCAAGGTCCCAGA	1440
QY	319	nGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLe	339
DB	1441	GGGCCCTTTACTGGACAAAAATTAAAGGACAAACATCCCTCTTGAGATGCTCAAGGAACTTGT	1500
QY	339	uArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIle-Gln-----	356
DB	1501	TCGTACTGATGGGGAACATCTCTTCAAGTTCCTCAATGCCCAAGTCATCAAAAGGTACTGC	1560
QY	356	-----	356
DB	1561	ATACATCTAACATCTTGTAATCTTTGAAGCCAGATTTATATATTTTTCGTAAAAAT	1620
QY	357	-----GluAspLysThrAlaTyrArgThrAspGluGluP	368
DB	1621	GATGACGTTTTTATCATGCTGGAGCAGAGGATAAGTCTGCATGGAGGACCGATGAAGAAT	1680
QY	368	heGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArg-----	383
DB	1681	TTGCAAGAGAAATGCTGGCTGGACTCAACCCAGTTGTTCATCCG-TCTACTCCAAGTAAAC	1739
QY	383	-----	383

Db 1740 TACAGCTTCCTTTCAAATAATTTTAAATGCCCTGTTGTTTCTTGAGAAAATGGAACCTTG 1799

QY 383 ----- 383

Db 1800 GAAAGGCTTCCAGACTTTGTTTCTTCTTCCCTCCATCTACTGTTCTTAGCTCTTTCTTGATA 1859

QY 384 -----LeuGlnGluPheProProLysSerLysLeuAspProL 396

Db 1860 ATTATTGGCTTTTCTACTTTGTTTGAGGAGTTTCTCCAAAAGCAAGCTGATCCTG 1919

QY 396 ysileTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspG 416

Db 1920 AAGTTTATGGCAACCAAAACAGTTCAATAACCAAGAACACATAGAGAAATCACCTGGATG 1979

QY 416 lyLeuThrIleAspGluAala----- 422

Db 1980 ACCTTACTATAAACGAGGT-AACGCTCTTAGGTTCCCTTCTTTTCAGACTAAATTTTCAA 2038

QY 422 ----- 422

Db 2039 TGTGACATGTTAATTTTGTGATTTGGAACACAGCCATAGTAACAGTGAATAATGGTGCTT 2098

QY 423 -----IleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetP 439

Db 2099 TTTACTAGGCAATGGAGAAGAGAGGCTATTTCATATTAGATCACCATGATGTTTTCATGC 2158

QY 439 roTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuL 459

Db 2159 CATACCTGAGGAGGATAAACACA---ACTTCCACGAAAACTTATGCCTCAAGGACTCTCC 2215

QY 459 euPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisP 479

Db 2216 TCTTCTGAAAGACGACGGAACCTTTGAAGCCACTGGCGATTGAATTGAGCCTACCACATC 2275

QY 479 roAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValG 499

Db 2276 CTAGTGGGGATAAATTTGGAGCTGTCAACAAAGTATATACGCCAGCTGAAAATGGTGTG 2335

QY 499 luGlySerIleTyrPheGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisG 519

Db 2336 AAGGTTCCATTGGCAGCTGGCTAAAGCTTATGCTGTGTGAATGACTCTGGCTATCATC 2395

QY 519 lnLeuIleSerHisTrpLeu----- 525

Db 2396 AGCTCCTCAGCCACTGGTA-TGTAATATCCCAAGGAAAGTGAATACAGTTTGGGCTTAA 2454

QY 526 -----AsnThrHisAlaAlaI 531

Db 2455 ATCTGAAGCGGTTGTGAATATCTTTTGATGTTGGTTGCAGGTTTGAATACACATGCTGCAA 2514

QY 531 leGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysL 551

Db 2515 TTGAGCCATTGTGATTGCAACCAACAGGCAGCTCAGCGTGCTTCATCCCAATTCACAAGC 2574

QY 551 euLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuI 571

Db 2575 TTTTGCATCCTCACTTCCGTGATACAATGAATGAATGAATGATGCTTAGCTCGACAAATCCTCA 2634

QY 571 leAsnGlyGlyLeuLeuGluLeuThrValPheProAlaLysTyrSerMetGluMets 591

Db 2635 TCAATGCTGGTGGAGTGGTGAGAGCACAGTTTTCATCAAAGTATGCCATGGAAATGT 2694

QY 591 erAlaValValTyrLysAspTrpValPheProGluGlnAlaLeuProThrAspLeuIleL 611

Db 2695 CATCTGTTGTTTACAAAGACTGGGTTCTTACTGAGCAAGCACTTCTCTGCTGATCTCATCA 2754

QY 611 ys----- 611

Db 2755 A-GAGGTATATAAATACTGTTAGTGATTGTTTCTTCTGCTGTGGAATGAATCTAGTG 2813

QY 612 -----ArgGlyVala 615

Db 2814 AAAATTGTGATTTTCATCTAACTGATATGCTGCAACTTGGGCACCTTTTCAGAGGAATGG 2873

QY 615 laValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrA 635

Db 2874 CGGTTGAGGATTCAGAGGCTCCTCATGGAAGTCCGCTACTGATAGATGACTACCCCTATG 2933

QY 635 laValAspGlyLeuLysIleTyrSerAlaIleLysSerTrpValThrGluTyrCysAsnT 655

Db 2934 CTGTTGATGGACTTGAGATCTGGTCAGCTATTGAGACATGGGTGAAAGAGTATTGCTCAT 2993

QY 655 yrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysG 675

Db 2994 TCTACTACAAGACAGATGAGATGGTCCAGAAAGACTCTGAGCTTCAGTCTGTGGTGAAGG 3053

QY 675 luLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnT 695

Db 3054 AAGTCAGGGAAGAGGTCATGGCGACAAGAGCAGCCCTGGTGGCTAAAATGCATA 3113

QY 695 hrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisA 715

Db 3114 CTGTCAAAGAGCTGATAGAAACATGCACCATTATCATCTGGTGGCTTCTGCTCTCCATG 3173

QY 715 laAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuS 735

Db 3174 CTGCAGTGAATTCGGGCAGTACCTTATGCAGGCTACCTCCCAAAACGCCCAACGATAA 3233

QY 735 erArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLysThrAsnProA 755

Db 3234 GCCGCAGATTTCATGCCTGAAGAAGGCACTCCTGAGTATGAAGAACTCAAGTCCAATCCTG 3293

QY 755 spLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuI 775

Db 3294 ATAAGGCTTTCCTGAAAACAATCACTGCCAGCTGCAGACCTTCTTGGCATCTCCCTTA 3353

QY 775 leGluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProG 795

Db 3354 TTGAGGTCCTTTCAGGCACTTCTCCGATGAGGTTTATCTTGGACAGAGAGACACTCCTG 3413

QY 795 luTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSera 815

Db 3414 AATGGACCTGGACACAACACCATTTGAAAGCTTTTGAGAAATTCGGAAGGAAGCTGGCAG 3473

QY 815 spIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyP 835

Db 3474 ACATTGAAGAATGATCATAGATAGAAATGGAATGAGAGATTCAAGAACAGAGTTGGGC 3533

QY 835 roValLysValProTyrThrLeuLeuPheProThrSerGluGlyGlyLeuThrGlyLysG 855

Db 3534 CTGTGAAGATACCATACACTGCTCTACCCCAAGGAAAGTGGGCTTACTGGCAAAG 3593

QY 855 lyIleProAsnSerValSerIle 862

Db 3594 GGATTCCTCAACAGTGTCTCCATC 3616

RESULT 5

US-09-978-522-2

; Sequence 2, Application US/09978522

; Patent No. 6787684

; GENERAL INFORMATION:

; APPLICANT: Descenzo, Richard

; APPLICANT: Ireland, Nancy

; TITLE OF INVENTION: Lipoxigenase Genes From Vitis Vinifera

; FILE REFERENCE: 29520/37890

; CURRENT APPLICATION NUMBER: US/09/978,522

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 60/241,220

; PRIOR FILING DATE: 2000-10-16

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 2

; LENGTH: 4687

; TYPE: DNA

; ORGANISM: Vitis LOX 1

US-09-978-522-2

Alignment Scores:

Pred. No.: 0 Length: 4687  
Score: 3138.00 Matches: 652  
Percent Similarity: 56.19% Conservative: 110  
Best Local Similarity: 48.08% Mismatches: 96  
Query Match: 69.21% Indels: 502  
DB: 4 Gaps: 10

US-10-731-642A-1 (1-862) x US-09-978-522-2 (1-4687)

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Db 13 CTTCTTTCAATTGTTAGTCCCATCACTGGGGAATGATAAGAAAGATCGAGGGAAC 72  
QY 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42  
Db 73 ATTGTGTTGATGAAGAAGAAATGTTGGATTTTAATGACTTCAATGCACCGGTTTCGGGAC 132  
QY 43 GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla 62  
Db 133 CGGGTTCATGAGCTTTTGGACAGGGAGTCTCTCGCAGCTCGTCAGTGTCTCATGGT 192  
QY 63 AspPro----- 64  
Db 193 GATCCTGGTGAGTTTTTTTTTTTTTTTTTTTTCCTTCATGTTTTTGATGGGTTGTTG 252  
QY 64 ----- 64  
Db 253 AAGTTGGAGGAGGAGGTTTGATACCGTTTTGTGTGAGGTTGAGATGGGTTCTGAATTTTGA 312  
QY 64 ----- 64  
Db 313 TGATAGCAATTGGAAAAAGATGTGATTTTGGAAAGAGGCCAAGAGGGGTTGTTATTCTCA 372  
QY 64 ----- 64  
Db 373 GAGATGAGTCAAAATGACTTTCTTGACATCTTCCATTCAACTGGGCACTTTCTAACTGCT 432  
QY 64 ----- 64  
Db 433 TTTGTTTTTTTGTTTTGTTTTTAATGCTTTTGTGTTTTTCTACTCTTCTCTGTTTATAT 492  
QY 64 ----- 64  
Db 493 TTCTTTTTCATCAACCACTATACATGCCCACTAACTCAATATGAATTTCCCATGCAGCTG 552  
QY 64 ----- 64  
Db 553 CCCTTTTTTAAAGCCCACTAGATCTTGGGTGATTTTTTAGTCTTAGATCTTGGGTTAGAT 612  
QY 64 ----- 64  
Db 613 TTCCCCAGATTTTCACAAAAAGTTGAAACTGAAATTCATAAAATTTTGGAGGATCACTCCTG 672  
QY 64 ----- 64  
Db 673 TTGGAGTTAAAGAGAAGAATTGGCCATAAACCAAGGAGATGAATTTGTGTGAATATTTC 732  
QY 64 ----- 64  
Db 733 TCAAAACCTTCATCAATAATACCTGCCAARAACAGCCACAGTTTCTGAAATTTTCATGCAGC 792  
QY 64 ----- 64  
Db 793 AAAGCCACTGCTGTTGTAGCAAGTCCAAGCTCAAAACATAAAAGCCTTTTCAACCCAGTG 852  
QY 64 ----- 64  
Db 853 ATTTTGTAGAAATAACATGTAAAAAATGCAGTGACCATCTGTTAGTGATGATATTGAACTTG 912  
QY 65 -----AlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAs 80

Db 913 TGTGCCTTTTTGTAGCAATGGTTACAGGGGAAACCTGGGAAACACAGCATACTTGGGAAGA 972  
QY 80 nTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAs 100  
Db 973 CTGGATTACCAACAATTACTTCTTTAACCGCTGGCGAGTGTGCATTCAAGGTCACGTTTCA 1032  
QY 100 pTrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSe 120  
Db 1033 CTGG---GATGAGGAGATTGGAGAGCCAGGGGCAATTCATAATTAGAAACAATCACCACAG 1089  
QY 120 rGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPh 140  
Db 1090 TGAGTTTACCTCAGGACTCTCACTCTTGAAGATGTTCTCGACGCTGGCAGAATTCACCTT 1149  
QY 140 eValCysAsnSerTirpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAl 160  
Db 1150 TGTTTGTAATTCCTGGGTCTACCTGCTAAGCACTACAAAAACTGACCGTGTTCCTTCAC 1209  
QY 160 aAsn----- 161  
Db 1210 TAATCAGGTAAGACTAATTTGCTTGATACTAGGAGAGTCTGCTGTGGCATTGTGGCCCAT 1269  
QY 162 -----GlnAl 163  
Db 1270 TGAGCTTAGGCAAGGAGAAATTGTCTGTCTAAAGGAATGTGTTATTTTATCTGCTGCAGAC 1329  
QY 163 aTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValTh 183  
Db 1330 ATATCTTCCAAGTGAAACACCCAGGGCCACTGCGCAAGTACAGAAAAAGGGAACACTGGTGAA 1389  
QY 183 rLeuArgGlyAspGlyThrGlyLysLeuGluGluTrpAspArgValTyrAspTyrAlaTy 203  
Db 1390 TCTGAGGGGAGATGGAACCCGAGAGCTTAAGGAATGGGATCGAGTGTATGACTATGCTTA 1449  
QY 203 rTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGl 223  
Db 1450 CTATAATGATTTGGGAAGCCAGACAGGGATCTCAAATATGCCCGCCCTGTGCTGGGAGG 1509  
QY 223 ySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys---- 241  
Db 1510 ATCTGCAGAGTATCCTTATCCAGGAGGGGAAGAACTGGTAGACCACCATCTGAAAAAGG 1569  
QY 241 ----- 241  
Db 1570 TAGATATTGTATACACAAATTCATATTGTTTCTCATGCTTTTATCATAAAGGATGAATA 1629  
QY 242 -----ThrAspProAsnSerGluSerArgIleProle 252  
Db 1630 TGATTGATTTCTGCTCTTCTTTTAATTAACAGATCCCAAAACTGAGAGCAGATTGCCACT 1689  
QY 252 uLeuMetSerLeuAspIleTyrValProArgAspGluArgPheGlyHisIleLysLeuSe 272  
Db 1690 TGTGATGAGCTTAAACATATATGTTCCAAGAGATGAACGATTTGGTCACTGAAGATGTC 1749  
QY 272 rAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLeuProGluPheLysAl 292  
Db 1750 AGACTTCCTGGCTTATGCCCTGAAATCCATAGTTCAATTCTCTCTGAGTTTGAGGC 1809  
QY 292 aLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLeuTyrGl 312  
Db 1810 TCTATGTGACATCACCCCAATGAGTTTGACAGCTTCCAAGATGTATTAGACCTCTACGA 1869  
QY 312 uGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIleProle 332  
Db 1870 AGGAGGAATCAAGGTCCAGAGGGCCCTTTACTGGACAAAAATTAAGGACAACATCCCTCT 1929  
QY 332 uGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrProThrPr 352  
Db 1930 TGAGATGCTCAAGGAACCTTGTTCGTACCGATGGGGAACATCTCTTCAAGTTCCCAATGCC 1989  
QY 352 oGlnValIle-Gln----- 356  
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Db 1990 CCAAGTCATCAAAGGTACTGCATACATCTAACATCTTGTAAATCTTTGAAGCCAGATTTAT 2049  
QY 357 -----GluAspLysThrA 361  
Db 2050 ATATTTATTTTCATAAAATTGATGACGTTTATCATGCTGGAGCAGAGGATAAGTCTG 2109  
QY 361 laTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleI 381  
Db 2110 CATGGAGGACTGACGAAGAATTTGCTAGAGAAATGCTGGCTGGAATCAACCCAGTTGTCA 2169  
QY 381 leSerArg----- 383  
Db 2170 TCCG-TCCTACTCCAAGTAAACTACAGCTTCCTTTCAAAATAATTTTAATGCCCTGTTGT 2228  
QY 383 ----- 383  
Db 2229 TTTCTGAGAAATGGAACCTTGGAAGGCTCCAGACTTTGTGTTTCTTCCCTCCATCTAC 2288  
QY 384 -----LeuGlnGluPheProp 389  
Db 2289 TGTTCTAGCTCTTTCTGATAAATTATTGGCTCTTTCTACTTTGTTGTAAGGAGTTTCCCTC 2348  
QY 389 roLysSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluG 409  
Db 2349 CAAAAGCAAGCTGGATCCTGAAGTTTATGGCAACCAACAGTTCAATAACCAAGAAC 2408  
QY 409 lnIleGluAspLysLeuAspGlyLeuThrIleAspGluAla----- 422  
Db 2409 ACATAGAGAATCACCTGGATGACCTTACTATAAACGAGGT-AACGCTCTTAGGTTCCGTT 2467  
QY 422 ----- 422  
Db 2468 CTTTCAACTAAATTTTCAATGTCGACATGTTAAATTTTGTGATTGGAACACAAGCCAT 2527  
QY 423 -----IleLysThrAsnArgLeuPheIleLeuA 432  
Db 2528 AGTAAGTGAATAATGGTGCTTTTACTAGGCAATGGAGAAGAGAGGCTATTTCATATTAG 2587  
QY 432 snHisHisAspIleLeuMetProTyrLeuArgArgIleAsnThrSerThrAspThrLysT 452  
Db 2588 ATCACCATGATGTTTTCATGCCATACCTGAGGAGGATAAACACA---ACTTCCACGAAAA 2644  
QY 452 hrTyrAlaSerArgThrLeuLeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaI 472  
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QY 472 leGluLeuSerLeuProHisProAspGlyAspGlnPheGlyAlaValSerLysValTyrT 492  
Db 2705 TTGAATTGAGCCTACCACATCCTTAATGGGATAAATTCGGAGTGTCAACAAAGTATACA 2764  
QY 492 hrProAlaAspGlnGlyValGluGlySerIleTyrGlnLeuAlaLysAlaTyrAlaAlaV 512  
Db 2765 CACCAGCTGAAGATGGCGTTGAAGTTCCATTTGGCAGCTGGCTAAAGCTTATGCTGCTG 2824  
QY 512 alAsnAspSerGlyValHisGlnLeuIleSerHisTrpLeu----- 525  
Db 2825 TGAATGACTCTGGCTATCATCAGCTCCTCAGCCACTGGTA-CGTAATCTCCCAAAGGAAA 2883  
QY 525 ----- 525  
Db 2884 GTGCTACAGTTGGGGCGTAAATCTGAAGCGGTTTATGAATATCTTTGATGTTGTTGCA 2943  
QY 526 -----AsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerA 544  
Db 2944 GGTGAATACACATGCTGCAATTGAGCCATTGTGATTGCAACCAACAGGCAGCTCAGTG 3003  
QY 544 laLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnA 564  
Db 3004 TGCTTCACCCCAATTCACAAGCTTTTGCATCCTCCTCATTCCGTCATGATGAATATAATG 3063  
QY 564 laLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuThrValPheProA 584  
Db 3064 CATTAGCTCGACAAATCCTCATCAATGCTGGTGGAGTGGTGGAGAGCACAGTTTTTCCAT 3123

QY 584 laLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPheProGluGlnA 604  
Db 3124 CAAAGTATGCCATGGAAATGTCTATCTGTTGTTTACAAAGACTGGGTCTCACTGAGCAAG 3183  
QY 604 laLeuProThrAspLeuIleLys----- 611  
Db 3184 CACTTCCTGCTGATCTCATCAA-GAGGTATATAAATACTGTGTAGTGATTTTCTTTTCC 3242  
QY 611 ----- 611  
Db 3243 TGCTGTGCAATGAATCTAGTGAATAATTGTGATTTTCATCTAACTGATATGCTCCAACCTG 3302  
QY 612 -----ArgGlyValAlaValGluAspSerSerSerProLeuGlyIleArgLeuL 628  
Db 3303 GGCACCTCTTTCAGAGGAATGGCGTTGAGGATTTCAGAGGCCCTCATGGACTCCGCCTAC 3362  
QY 628 euIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTyrSerAlaIleLysSert 648  
Db 3363 TGATAGATGACTACCCCTATGCTGTGTGATGGACTTGAGATCTGGTCAGCTATTGAGACAT 3422  
QY 648 rpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAspAlaValGlnLysAspThrG 668  
Db 3423 GGGTGAAAGAGTATTGCTCATCTACTACAAGACAGATGAGATGGTCCAGAAAGACTCTG 3482  
QY 668 luLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHisGlyAspLysLysAspGluP 688  
Db 3483 AGCTTCAGTCTCTGGTGAAGGAAGTTCAGGGAAGAGGGTTCATGGCGACAAGAGGACGAGC 3542  
QY 688 roTrpTrpProLysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIleT 708  
Db 3543 CTTGTGGCCTAAATGCGTACTGTCAAAGAGCTGATAGAAACATGCACCATTTATCATCT 3602  
QY 708 rpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrL 728  
Db 3603 GGGTGGCTTCTGCTCTCCATGCTGCAGTGAAATTTTCGGGCGATACCTTATGCAGGCTACC 3662  
QY 728 euProAsnArgProThrLeuSerArgAsnPheMetProGluProGlySerProGluTyrG 748  
Db 3663 TCCCAAAACCGCCCAACGATAAGCCGACAGATTTCATGCTTGAAAGAGCACCTCCTGAGTATG 3722  
QY 748 luGluLeuLysThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGlnT 768  
Db 3723 AAGAACTCAAGTCCAATCCTGATAAGGCTTTCTGTGAAAAAATCACTGCCCAGCTGCAGA 3782  
QY 768 hrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHisSerSerAspThrLeuTyrL 788  
Db 3783 CCCTTCTTGGCATCTCCCTTATTGAGGTCCCTTCCAGGCATTTCTCCGATGAGGTTTATC 3842  
QY 788 euGlyGlnArgGluSerProGluTyrThrLysAspGlnGluProLeuSerAlaPheAlaA 808  
Db 3843 TTGCACAGAGAGACACTCCTGATGGACCCCTGGACACACACACCATTTGAAAGCTTTTGAGA 3902  
QY 808 rgPheGlyLysLysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGluL 828  
Db 3903 AATTGGAAGGAAGCTGGCAGACATTGAAGAAATGATCATAGATAGAAATGGAAATGAGA 3962  
QY 828 ysTrpLysAsnArgSerGlyProValLysValProTyrThrLeuLeuPheProThrSerG 848  
Db 3963 GATTCAAGAACAGAGTTGGGCCTGTGAAGATACCATACACTGCTCTACCCCAAGCG 4022  
QY 848 luGlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862  
Db 4023 AAGGTGGGCTTACTGGCAAAGGGGATTCCCAACAGTGTCTCCATC 4066

RESULT 6

US-09-810-268-2  
; Sequence 2, Application US/09810268  
; Patent No. 6627797  
; GENERAL INFORMATION:  
; APPLICANT: Duvick, Jon  
; APPLICANT: Maddox, Joyce R.  
; APPLICANT: Keller, Nancy P.

; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Zea mays
US-09-810-268-2

Alignment Scores:
Pred. No.: 3.86e-301 Length: 2595
Score: 2779.50 Matches: 525
Percent Similarity: 74.86% Conservative: 124
Best Local Similarity: 60.55% Mismatches: 207
Query Match: 61.30% Indels: 11
DB: 4 Gaps: 5

US-10-731-642A-1 (1-862) x US-09-810-268-2 (1-2595)

QY 3 LeuGluLysIleValAspAlaIleThrGlyLysAspAspGlyLysLysValLysGlyThr 22
Db 4 CTGAGCGGATCATCGACGGGCTGACGGGGGGAACAAGCATGCGCGGCTCAAGGGCACG 63
QY 23 ValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerValLeuAsp 42
Db 64 GTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGGCACCGTCTGTGAC 123
QY 43 GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla 62
Db 124 AGCATCAGCGAGTTCCTCGCAAGGGGTACCTGCCAGCTCATCAGCTCCACCCTCGTC 183
QY 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82
Db 184 GACGCCAACACCGCAACCGCGGGGGTCTGGGGCGGAGGCGAACCTGGAGCAGTGGCTG 243
QY 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
Db 244 ACGAGCCTGCCGTGCTGACGACCGCGGAGTCCAAAGTTCGGCGTCACGTTCCGACTGGAG 303
QY 103 AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122
Db 304 GTGGAGAAGCTGGGAGTCCCGGGCCGTCGTCGTCGAAGAACAACCAACCGCGCGAGTTC 363
QY 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
Db 364 TTCCTCAAGACAATCACCTCGACGACGTGCCCGCGCGCGCGTCACTTCGTCGCC 423
QY 143 AsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePheAlaAsnGln 162
Db 424 AACTCCTGGGTCTACCCCGCGGCAAGTACCGGTACAACCGCGTCTTCTTCCAAACGAT 483
QY 163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182
Db 484 ACGTACCTGCCAAGCCAGATGCCGGCGGCGTGAAGCCGTACCGCAGCAGCTCCGC 543
QY 183 ThrLeuArgGlyAspGly---ThrGlyLysLeuGluGluTrpAspArgValTyrAspTyr 201
Db 544 AACCTCCGCGCGCAGCAGCAGCAGGGCCCTACCAGGAGCAGCAGCCGCGTGTACCGCTAC 603
QY 202 AlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeu 221
Db 604 GACGTCTACAACGACCTCGCGGAGCCCGACGGCGGCAAC-----CGCGCGCCCATCTC 657
QY 222 GlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLys 241
Db 658 GCGGGCTCCGCCGACCAACCCGTACCCCGCGCGCTGCGCGCAGCGGGCCGAAGCCACCAA 717

QY 242 ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValPro 261
Db 718 ACCGACCCCAACTCGGATAGCGACTGTCTGGTGGAG-----CAGATCTACGTGCCG 771
QY 262 ArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSer 281
Db 772 CGGGACGAGCGCTTCGGCCACCTCAAGATGTCCGACTTCTCTGGGCTACTCCATCAAGGCC 831
QY 282 IleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPhe 301
Db 832 ATCACCAGGGCATCATCCCGGGGTGCGCACGCTACGTGGACACCAACCCGGCGAGTTC 891
QY 302 AspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuProGlnGlyPro 321
Db 892 GACTCCTCCAGGACATCATCACTGTACGAGGGCGGGATCAAGCTGCCCCAAGATCCAG 951
QY 322 LeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSer 341
Db 952 GCGCTCGAGGACATCGCAAGCTCTTCCCGTCCAGTCCGTCGTCGTCGTCGTCGTCGTCG 1011
QY 342 AspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAla 361
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QY 382 SerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyrGlyAsnGln 401
Db 1132 ACGGCGCTCAGGAGTTCGCGGCCCAAGAGCAGCGTGGACCCCAAGTACGGCGACCAC 1191
QY 402 AsnSerThrIleThrArgGluGlnIleGluAspLysLeuAspGlyLeuThrIleAspGlu 421
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QY 442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461
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QY 462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481
Db 1372 CGCGGGACGGCAGGCTCGCGCCCTCGCCATCGAGCTCAGCGAGCGGTACATCGACGGG 1431
QY 482 AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501
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QY 502 IleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyValHisGlnLeuIle 521
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QY 522 SerHisTrpLeuAsnThrHisAlaAlaIleGluPropheValIleAlaThrAsnArgGln 541
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QY 542 LeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsn 561
Db 1612 CTGAGCGTGCACGACCCCGGTGCACAAGTCTCTGAGCTCGCAGCTTCCCGCAGACCATGACC 1671
QY 562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeuThrVal 581
Db 1672 ATCAACGCGCTGGCGGGCAGACGCTCATCAACGGCGGGCGGTCATCTTCGAGATGACCGTC 1731
QY 582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhePro 601
Db 1732 TTCCCGGGCAAGTACGGCGTGGGCATGTCTCCGTGGTGTACAAGAGCTGGAACCTTCACC 1791
QY 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSer 621

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Db 1792 GAGCAGGGCCTCCCGCCGACCTCGTCAAGAGGGCGTGGCGGTGGCGACCCGTCACG 1851
QY 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIle 641
Db 1852 CCGTACAAGGTGGCGTGTGATCGAGGACTACCGGTACGGAGCGACGGGCTGGCCATC 1911
QY 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAsp 661
Db 1912 TGGCAGCCCATCGAGCAGTGGTGGCGAGTACTGGCCATCTACTACCCGACGACGGC 1971
QY 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGlyHis 681
Db 1972 GCGCTGCGGGGCGACGAGGAGCTGCAGCGTGTGTGAAGGAGGTGCGCGAGGTGCGGCAC 2031
QY 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701
Db 2032 GCGCACCACAAGACGCGCCCTGTTGGCCCAAGATGCAGGCCGTGTCTCGAGCTCGCCAGC 2091
QY 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGln 721
Db 2092 GCCTGCACCACCATCATCTGGATCGCGTCCGCGCTCCACGCCCGCTCAACTTCGGCCAG 2151
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QY 742 ProGlySerProGluTyrGluLeuLysThrAsnProAspLysValPheLeuLysThr 761
Db 2212 CCCGGCAGCAAGGAGTACGAGGAGCTGGAGCGCGACCCGAGCGCGGCTTCATCCACACC 2271
QY 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781
Db 2272 ATCACGAGCCAGATCCAGACCATCATCGGCATCTCGCTCATCGAGATCCTCTCCAAGCAC 2331
QY 782 SerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTyrTrpLysAspGlnGlu 801
Db 2332 TCCTCCGACGAGGTGTACCTCGGCCAGCGCGACACCCCGAGTGGACCTCCGACGCCCGG 2391
QY 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821
Db 2392 GCGCTGGCGGGCTTCAAGAGGTTTCAGCGACGCGCTGGTCAAGATCGAGGCGAAGTGGTG 2451
QY 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841
Db 2452 GCGGAGAACCGGACCCGACCGCAGCTGAGGAACAGGAACGGCCCCCGCGAGTTCCCTACATG 2511
QY 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855
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RESULT 7
US-09-810-268-1
; Sequence 1, Application US/09810268
; Patent No. 6627797
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jon
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Keller, Nancy P.
; TITLE OF INVENTION: Maize Lipoxigenase Polynucleotide and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 1269
; CURRENT APPLICATION NUMBER: US/09/810,268
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,950
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
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; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Zea mays
US-09-810-268-1
Alignment Scores:
Pred. No.: 4.98e-301 Length: 3007
Score: 2779.50 Matches: 525
Percent Similarity: 74.86% Conservative: 124
Best Local Similarity: 60.55% Mismatches: 207
Query Match: 61.30% Indels: 11
DB: 4 Gaps: 5
US-10-731-642A-1 (1-862) x US-09-810-268-1 (1-3007)
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Db 128 GTGGTGTCTATGCGCAAGAACGTGTGTGACCTCAACGACTTCGGCGCCACCGTCTGTGAC 187
QY 43 GlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerValAsnAla 62
Db 188 AGCATCAGCGAGTTCTTCGGCAAGGGGTACCTGCCAGCTCATCAGCTCCACCTCGTC 247
QY 63 AspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsnTrpLeu 82
Db 248 GACGCCAACAAACGGCAACCCGCGGGCGGTTCGGGGCGGAGGCGAACCCTGGAGCAGTGGCTG 307
QY 83 ThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAspTrpAsp 102
Db 308 ACGAGCTCGCGTCTGCTGACGACCGCGGAGTCCAAGTTCGGCGTCAAGTTCGACTGGGAG 367
QY 103 AspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSerGluPhe 122
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QY 123 PheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHisPheValCys 142
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QY 163 AlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuVal 182
Db 548 ACGTACCTGCCAAGCCAGATGCCCGCGCGCTGAAGCCGTACCGCGACGACGAGTCCGC 607
QY 183 ThrLeuArgGlyAspGly--ThrGlyLysLeuGluGluTyrAspArgValTyrAspTyr 201
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QY 242 ThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValPro 261
Db 782 ACCGACCCCAACTCGGATAGCCGACTGCTGCTGGTGGAG-----CAGATCTACGTGCCG 835
QY 262 ArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSer 281
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QY 282 IleValGlnLeuLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPhe 301
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Db 956 GACTCCTTCCAGGACATCATCAACCTGTACGAGGGCGGATCAAGCTGCCAAGATCCAG 1015

Qy 322 LeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSer 341

Db 1016 GCGCTCGAGGACATGGCGAAGCTCTTCCCGCTCCAGCTCGTCAAGGACCTCTCCCGCC 1075

Qy 342 AspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAspLysThrAla 361

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Qy 362 TrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIle 381

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Db 1256 ACCAGCACGATCACGGCGGAGCACATCGAGAAGAACCTCGAGGGCTCACGGTGCAGCAG 1315

Qy 422 AlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMetProTyrLeu 441

Db 1316 GCGCTGGAGCGCAACAGGCTCTACATCTCTGACCACCAACGACCGCTTCATGCCGTTCTC 1375

Qy 442 ArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeuLeuPheLeu 461

Db 1376 ATCAGCGTCAACAACTGGAGGGCAACTTATCTACGCCACCAAGGACGCTCTTCTTCCTG 1435

Qy 462 GlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGly 481

Db 1436 CGCGGGACGGCAGGCTCGCGCCCTCGCCATCGAGCTCAGCGAGCGGTATCATCGACGGG 1495

Qy 482 AspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySer 501

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Db 1676 CTGAGCGTGACGACCCCGGTGCACAAGCTCTGAGCTCGCACTTCCGCGACACCATGACC 1735

Qy 562 IleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGluLeuThrVal 581

Db 1736 ATCAACGCGCTGGCGCGGCGAGACGCTCATCAACGCGCGCGGCATCTTCGAGATGACCGTC 1795

Qy 582 PheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPhePro 601

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Qy 602 GluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSer 621

Db 1856 GAGCAGGGCCCTCCCGCCGACCTCGTCAAGAGGGCGTGGCGGTGGCGGACCCGTCACGC 1915

Qy 622 ProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIle 641

Db 1916 CCGTACAAGGTGGCGCTGCTGATCGAGGACTACCCGTACGCGAGCGAGCGGTGGCCATC 1975

Qy 642 TrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAsp 661

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Qy 662 AlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHis 681

Db 2036 GCGTCGCGGGCGACGAGGAGCTGCAGCGGTGGTGAAGGAGGTGCGGAGGTTCGGGCAC 2095

Qy 682 GlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAsp 701

Db 2096 GCGACCAACAAGGACGCGCCCTGGTGGCCCAAGATGCAGCGCGTGTGCGAGCTCGCCAGC 2155

Qy 702 SerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaValAsnPheGlyGln 721

Db 2156 GCCTGCACCAACCATCATCTGGATCGCTCGGCGTCCACGCGCGCTCAACTTCGGCCAG 2215

Qy 722 TyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetProGlu 741

Db 2216 TACCGTACGCGGGTACCTCCGAAACAGGCCACCGTGAGCGCGCGGATGCCGAG 2275

Qy 742 ProGlySerProGluTyrGluLeuLysThrAsnProAspLysValPheLeuLysThr 761

Db 2276 CCGGAGCAAGGAGTACGAGGAGCTGGAGCGGACCCCGGAGCGCGGCTTCATCCACACC 2335

Qy 762 IleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHis 781

Db 2336 ATCAGAGCCAGATCCAGACCATCATCGGCATCTCGTCTCATCGAGATCCTCTCCAAGCAC 2395

Qy 782 SerSerAspThrLeuTyrLeuGlnArgGluSerProGluTrpThrLysAspGlnGlu 801

Db 2396 TCCTCGACGAGGTGTACCTCGGCGAGCGGACACCCCGAGTGGACCTCCGACGCCCGG 2455

Qy 802 ProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGluAspGlnIleMet 821

Db 2456 GCGTGGCGGCGTTCAAGAGGTTTCAGCGACGCGCTGGTCAAGATCGAGGGCAAGGTGGTG 2515

Qy 822 GlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLysValProTyrThr 841

Db 2516 GCGGAGAACCAGCCCCGACGCTGAGGAACAGGAACGCGCCCGCGAGTTCCTTACATG 2575

Qy 842 LeuLeuPhePro---ThrSerGlu-----GlyGlyLeuThrGlyLysGly 855

Db 2576 CTGCTCTATCCCAACACCTCTGACCACAGTGGCGCGCGCGGCTCACTGCCAAGGGC 2635

Qy 856 IleProAsnSerValSerIle 862

Db 2636 ATCCCCAACAGCATCTCCATC 2656

RESULT 8

US-09-751-687-10  
; Sequence 10, Application US/09751687  
; Patent No. 6660915  
; GENERAL INFORMATION:  
; APPLICANT: Douma, Anneke  
; APPLICANT: Doderer, Albert  
; APPLICANT: Cameron-Mills, Verena  
; APPLICANT: Skadhauge, Birgitte  
; APPLICANT: Bech, Lene  
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY  
; FILE REFERENCE: 11225.11US01  
; CURRENT APPLICATION NUMBER: US/09/751,687  
; CURRENT FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 2818  
; TYPE: DNA  
; ORGANISM: Hordeum vulgare  
US-09-751-687-10

Alignment Scores:  
Pred. No.: 6.64e-290 Length: 2818  
Score: 2680.00 Matches: 502  
Percent Similarity: 73.25% Conservative: 136  
Best Local Similarity: 57.63% Mismatches: 215  
Query Match: 59.11% Indels: 18

DB: 4 Gaps: 7  
US-10-731-642A-1 (1-862) x US-09-751-687-10 (1-2818)  
QY 1 MetPheLeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysValLys 20  
DB 69 ATGCTGCTGGAGGGCTGATGCACACCTCACGGGGCGGAACAAGAGCGCCGGCTCAAG 128  
QY 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40  
DB 129 GGCACGGTGGTCTCATGCGAAGAACGTCTGGACCTCAACGACTTCGGCGCCACCATC 188  
QY 41 LeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerVal 60  
DB 189 ATCAGCGGCATCGGCGAGTTCCTCGGCAAGGGCGTCACTGCCAGCTTATAGTCCACC 248  
QY 61 AsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGluAsn 80  
DB 249 GCCGTCGACCAAGACAACGGCGGTTCGGGGAAGTGGGCGCGGAGCGGAGCTGGAGCAG 308  
QY 81 TrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPheAsp 100  
DB 309 TGGGTGACGAGCCTGCGCTGCTGACGACGGGGAGTCCAAGTTCGGCCTCACCTTCGAC 368  
QY 101 TrpAspAspGluGluPheGlyValProGlyAlaPheIleIleLysAsnLeuHisPheSer 120  
DB 369 TGGGAGGTGGAGAAGCTCGGGTGCCGGCGCCATCGTCTGTCACAACACTACCACAGCTCC 428  
QY 121 GluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis---GlyLysValHis 139  
DB 429 GAGTTCCTGCTTAAACCATCACCTCCACGACGTCCCCGGCGGACGGCAACCTCAC 488  
QY 140 PheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePhe 159  
DB 489 TTCGTGCGCAACTCATGGATCTACCCCGCGCCAACTACCGATACAGCCGCTTCTTTC 548  
QY 160 AlaAsnGlnAlaTyrLeuProSerGluThrProAspThrLeuArgLysTyrArgGluAsn 179  
DB 549 GCCAACGACACGTACTCGCGAGCCAGATGCGCGGGCGGTGAAGCCGTACCGCGACGAC 608  
QY 180 GluLeuValThrLeuArgGlyAspGly---ThrGlyLysLeuGluGluTrpAspArgVal 198  
DB 609 GAGCTCCGGAACCTGCGTGGCGACGACCAGCGGCCGTACCAGGAGCAGCAGCGCATC 668  
QY 199 TyrAspTyrAlaTyrTyrAsnAspLeuGlyAspProAspLysGlyGlnAspLeuSerArg 218  
DB 669 TACCGCTACGCGCAACTCCGACCACTCGGCGAG-----GGCCGC 707  
QY 219 ProValLeuGlyGlySerSerGluTyrProTyrProArgArgGlyArgThrGlyArgLys 238  
DB 708 CCCATCCTCGGCGCAACTCCGACCACTTACCCCGCGCGCTGCTGGAG-----CAGATC 767  
QY 239 ProThrLysThrAspProAsnSerGluSerArgIleProLeuLeuMetSerLeuAspIle 258  
DB 768 CCCAACGCCAGCACCCCGAGCCTGGAGAGCGCGCTGCTGGAG-----CAGATC 821  
QY 259 TyrValProArgAspGluArgPheGlyHisIleLysLeuSerAspPheLeuThrPheAla 278  
DB 822 TACGTGCCGCGGACGAGAAGTTCGGCCACCTCAAGACGTCGACCTTCTGGGCTACTCC 881  
QY 279 LeuLysSerIleValGlnLeuLeuLeuProGluPheLysAlaLeuPheAspSerThrHis 298  
DB 882 ATCAAGGCCATCAGCAGGGGCATCCTGCGCGCGGTGGCACCTACGTGGACACCAACCCC 941  
QY 299 AsnGluPheAspSerPheGluAspValLeuLysLeuTyrGluGlyGlyIleLysLeuPro 318  
DB 942 GCGAGTTCGACTCCTTCCAGGACATCATCAACTCTATAGGGCGCGCATCAAGCTGCCC 1001  
QY 319 GlnGlyProLeuLeuLysAlaIleThrAspSerIleProLeuGluIleLeuLysGluLeu 338  
DB 1002 AAGGTGGCCCGCTCGAGGAGCTCCGTAAGCAGTTCCTCCGCTCCAGCTCATCAAGGACCTC 1061  
QY 339 LeuArgSerAspGlyGluGlyLeuPheLysTyrProThrProGlnValIleGlnGluAsp 358

DB 1062 CTCCCCGTGCGGCGGACTCCCTTGCTTAAGCTCCCCGTGCCCCACATCATCCAGGAGAAC 1121  
QY 359 LysThrAlaTrpArgThrAspGluGluPheGlyArgGluMetLeuAlaGlyValAsnPro 378  
DB 1122 AAGCAGCGCTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCGCGCTCAACCCG 1181  
QY 379 ValIleIleSerArgLeuGlnGluPheProProLysSerLysLeuAspProLysIleTyr 398  
DB 1182 GTCATGATCAGCGCTCTCACGGAGTTCGCGCCAAAAAGTAGTCTGGACCTTAGCAAGTTT 1241  
QY 399 GlyAsnGlnAsnSerThrIleThrArgGluGlnIleGluAspLysLysLeuAspGlyLeuThr 418  
DB 1242 GGTGACCAACACAGCACCATCATCAGCGGAGACACATAGAGAAGAACCTCGAGGGCCTCACG 1301  
QY 419 IleAspGluAlaIleLysThrAsnArgLeuPheIleLeuAsnHisHisAspIleLeuMet 438  
DB 1302 GTGCAGCAGGCGCTGGAAGCAACAGGCTGTACATCCTTGATCACCATGACCGGTTCATG 1361  
QY 439 ProTyrLeuArgArgIleAsnThrSerThrAspThrLysThrTyrAlaSerArgThrLeu 458  
DB 1362 CCGTTCCTGATCGACGTCAACAACCTGCGCGGCAACTTCATCTACGCCACGAGGACCTC 1421  
QY 459 LeuPheLeuGlnAspAsnGlyThrLeuLysProSerAlaIleGluLeuSerLeuProHis 478  
DB 1422 TTCTTCTGCGGCGGCGAGCGGTTCACGCCGCTCGCCATCGAGTGAGCGAGCCCATC 1481  
QY 479 ProAspGlyAspGlnPheGlyAlaValSerLysValTyrThrProAlaAspGlnGly--- 497  
DB 1482 ATCCAGSGCGGCTTACCACGGCCAAAGAGCAAGTTTACACGCCGCTGCCAGCGGCTCC 1541  
QY 498 ValGluGlySerIleTrpGlnLeuAlaLysAlaTyrAlaAlaValAsnAspSerGlyVal 517  
DB 1542 GTCGAAGGCTGGGTGTGGAGCTCGCCAAGGCCTACGTGCGCGTCAATGACTCCGGGTGG 1601  
QY 518 HisGlnLeuIleSerHisTrpLeuAsnThrHisAlaAlaIleGluProPheValIleAla 537  
DB 1602 CACCAGCTGTCAGCCACTGGCTGAACACTCACGCGGTGATGGAGCCGTTCGTGATCTCG 1661  
QY 538 ThrAsnArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArg 557  
DB 1662 ACGAACCGGCACCTTAGCGTGACGACCCGGTGACAAGCTGCTGAGCCCGCACTACCGC 1721  
QY 558 GluThrMetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeu 577  
DB 1722 GACACCATGACCATCAACGCGCTGGCGCGGACGCTCATCAACGCCGCGGCATCTTC 1781  
QY 578 GluLeuThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAsp 597  
DB 1782 GAGATGACGGTGTTCGCGGCAAGTTCGCGTTGGGATGTGCGGCGGTGTTACAAGGAC 1841  
QY 598 TrpValPheProGluGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGlu 617  
DB 1842 TGGAGTTTACCGAGCAGGACTGCGCGACGATCTCATCAAGAGGGGATGGCGGTGGAG 1901  
QY 618 AspSerSerSerProLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAsp 637  
DB 1902 GACCCGTCGAGCCCGTACAAGGTGCGGTGCTGGTGTGCGACTACCCGTACGCGCGGAC 1961  
QY 638 GlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyr 657  
DB 1962 GGGCTGGGATCTGGCAGCGCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTAC 2021  
QY 658 LysSerAspAspAlaValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArg 677  
DB 2022 CCGAAGCAGCGCGTGTGTCAGGGCGATACGGAGGTGCAGCGCTGGTGGAGGAGACCGCG 2081  
QY 678 GluGluGlyHisGlyAspLysLysAspGluProTrpTrpProLysMetGlnThrValGln 697  
DB 2082 GAGGTGGGCACGGCGACCTCAAGGACGCCCATGGTGGCCCAAGATGCAAGTGTGCCG 2141  
QY 698 GluLeuIleAspSerCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaAlaVal 717

Db 2142 GAGCTGGCCAAAGCGTGCACCAACCATCTGTGATCGGGTCGGCGTGCATCGGCAGTC 2201  
QY 718 AsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsn 737  
Db 2202 AACTTCGGGAGTACCCCTACGCGGGGTTCCTCCCGAACCGGCCGACGGTGAGCCGGCGC 2261  
QY 738 PheMetProGluProGlySerProGluTyrGluLeuLysThrAsnProAspLysVal 757  
Db 2262 CGCATGCCGAGCCCGGCACGGAGGAGTACGGGAGCTGGAGCGGACCCGGAGCGGGCC 2321  
QY 758 PheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGlyLysLeuIleGluIle 777  
Db 2322 TTCATCCACACCATCACGAGCCAGATCCAGACCATCATCGGCGTGTGCTGTGGAGTG 2381  
QY 778 LeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArgGluSerProGluTrpThr 797  
Db 2382 CTGTGGAAGCACTCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGACC 2441  
QY 798 LysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleGlu 817  
Db 2442 TCGGACCCCAAGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGAGATCGAG 2501  
QY 818 AspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLys 837  
Db 2502 AGCAAGGTGGTGGCATGAACCATGACCCCGGAGCTCAAGAACCCGCAACGCCCGGCTAAG 2561  
QY 838 ValProTyrThrLeuLeuPhePro---ThrSerGlu-----GlyGlyLeu 851  
Db 2562 TTTCCCTACATGCTGCTCTACCCCAACACTCCGACCACAAGGGCGCGCTGCCGGGCTT 2621  
QY 852 ThrGlyLysGlyIleProAsnSerValSerIle 862  
Db 2622 ACCGCCAAGGCATCCCCAACACAGCATCTCCATC 2654

RESULT 9

US-09-751-687-8  
; Sequence 8, Application US/09751687  
; Patent No. 6660915  
; GENERAL INFORMATION:  
; APPLICANT: Douma, Anneke  
; APPLICANT: Doderer, Albert  
; APPLICANT: Cameron-Mills, Verena  
; APPLICANT: Skadhauge, Birgitte  
; APPLICANT: Bech, Lene  
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY  
; FILE REFERENCE: 11225.11US01  
; CURRENT APPLICATION NUMBER: US/09/751,687  
; CURRENT FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 4663  
; TYPE: DNA  
; ORGANISM: Hordeum vulgare  
US-09-751-687-8

Alignment Scores:  
Pred. No.: 1.15e-244 Length: 4663  
Score: 2280.50 Matches: 504  
Percent Similarity: 45.89% Conservative: 138  
Best Local Similarity: 36.03% Mismatches: 211  
Query Match: 50.30% Indels: 548  
DB: 4 Gaps: 14

US-10-731-642A-1 (1-862) x US-09-751-687-8 (1-4663)

QY 1 MetPheLeuGluLysIleValAspAlaIleThrGlyLysAspGlyLysLysValLys 20  
Db 357 ATGCTGTGGAGGGGTGATCGACACCCCTACGGGGCGGAACAAGAGCGCGGCTCAAG 416  
QY 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40  
pb 417 GGCACGGTGGTGTCTCATGCGCAAGAACGCTGTGGACCTCAACGACTTCGGCGCCCAACATC 476

QY 41 LeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerVal 60  
Db 477 ATCGACGGCATCGGCGAGTTCCTCGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC 536  
QY 61 -----AsnAlaAspProAlaAsnGlyLeu----- 68  
Db 537 GCGTCGACCAAGGTAATCACTA-CCCTCCTCGGCCTTCCTCTGTTTACAAGATATA 595  
QY 68 ----- 68  
Db 596 GTATTCTTTCGTGTGGGCCGGGCCCATGGATGGATGTGTCTGGATCGGCTAAAG 655  
QY 68 ----- 68  
Db 656 AAGATAGGATAGCTAGCCCTGGCCGGTCGTCTTTACCTGACATGGGCATATGCCATCGA 715  
QY 68 ----- 68  
Db 716 AAAAAAGAGACAACAGCATGCATGCTGTCGGCGCACCCAGACGACGCCGGATG 775  
QY 68 ----- 68  
Db 776 CTCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAAGCAACAACAAGCAAG 835  
QY 68 ----- 68  
Db 836 GACGGCACGTCAAAAGCAACAAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCAC 895  
QY 68 ----- 68  
Db 896 ACAATCAGCAGGCTATAAAACAGTTGTTCATCAAAAACAACGCTGGAAGAGAGAGAAGGA 955  
QY 68 ----- 68  
Db 956 AGGAAGTAGTAGCCATGAAAAATAAATCAACCGGGCGTTGCTCTTTGCCCAACAATTAT 1015  
QY 68 ----- 68  
Db 1016 CAAGCAGGGTACGTGGCATGTATAGTTCTTGTAACTAAGCATGTGATATGAGAAG 1075  
QY 69 -----GlnGlyLysArgSerLysAlaAlaTyrLeuGlu 79  
Db 1076 GTACGTGGTGTGCAGACAACGGCGGTTCGGGAAGGTGGCGCGGAGCGGAGTGGAG 1135  
QY 80 AsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPhe 99  
Db 1136 CAGTGGGTGACGAGCCTGCGCTGCTGACGACGGGGGAGTCCAAAGTTCGGCCTCACCTTC 1195  
QY 100 AspTrpAspAspGluGluPheGlyValProGlyAlaPheIleLysAsnLeuHisPhe 119  
Db 1196 GACTGGGAGGTGGAGAAGCTCGGGGTGCGGGCGCCATCGTCCTCAACAACACTACCACAGC 1255  
QY 120 SerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHis---GlyLysVal 138  
Db 1256 TCCGAGTTCCTGCTTAAACCATCACCTCCACGACGTCCTCCCGCGCGCAGCGCAACCTC 1315  
QY 139 HisPheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhe 158  
Db 1316 ACCTTCGTCGCCAAACTCATGGATCTACCCCGCCCAACTACCGATACAGCCGCGTCTTC 1375  
QY 159 PheAlaAsn----- 161  
Db 1376 TTCGCCAACGACGTCGCTGAATTTCTCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1435  
QY 161 ----- 161  
Db 1436 CGTCATTTCATGGTCGATCATTAAGTCTTCCAGGACAATAGATGATGAGCTAGGAGTGGT 1495  
QY 161 ----- 161  
Db 1496 TACCACCTAGCAGTACGTACATTATTATTTCGGTGTGGTAGAAAAAGGATATGGTTTGGT 1555



QY	161	-----	161
Db	1556	GCAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCGTGGCAGCGTGGTAGGTG	1615
QY	161	-----	161
Db	1616	AAAATAACTGTTGCACGGATCCACCCACATGATTGTTTTCATGAATAAACTTTTAAAGGA	1675
QY	161	-----	161
Db	1676	TGTGTCTAGCCACATCTAGATGCATGTACATAATTATTATGTCATACCAAAACGATTAAATT	1735
QY	161	-----	161
Db	1736	AAGCATAAAAAAGAAAAGGAAAAAATACTACATATCTCGACGTAAGATCAATGATATAG	1795
QY	161	-----	161
Db	1796	TATTTAGATATGCAATATTATTCTTACATCTAAACCTTTCTTCATTCTTAAATATAAGAC	1855
QY	161	-----	161
Db	1856	ATTTGTAAGATTTCACTATGGAACAACATACGAAACAAAATCAGTGGATCTCTCTATGCAT	1915
QY	161	-----	161
Db	1916	TCATTATGTAGTCTAATAAATAAATCTTTAAAGATCGTATATTTTGCAACGGAGGAGTA	1975
QY	162	-----	167
Db	1976	AAACATAACTTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTAACCTGCCGAG	2035
QY	167	rGluThrProAspThrLeuArgLysTyrArgGluAsnGluLeuValThrLeuArgGlyAs	187
Db	2036	CCAGATGCCGGCGGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGGCGGA	2095
QY	187	pGly--ThrGlyLysLeuGluGluTrpAspArgValTyrAspTyrAlaTyrTyrAsnAs	206
Db	2096	CGACCAGCAGGGCCGTACGAGGAGCAGCACCAGCATCTACCGCTACGACGCTCTACAACGA	2155
QY	206	pLeuGlyAspProAspLysGlyGlnAspLeuSerArgProValLeuGlyGlySerSerG1	226
Db	2156	CCTCGGCGAG-----GGCCGCCCCCATCTCTCGCGGGCAACTCCGA	2194
QY	226	uTyrProTyrProArgArgGlyArgThrGlyArgLysProThrLysThrAspProAsnSe	246
Db	2195	CCACCCTTACCCGCGCGCGCGCCGACGAGGCGCAAGCCCAACGCCAGCGACCCGAGCCT	2254
QY	246	rGluSerArgIleProLeuLeuMetSerLeuAspIleTyrValProArgAspGluArgPh	266
Db	2255	GGAGAGCCGGCTGTCTGCTGGAG-----CAGATCTACGTCCCGCGGACGAGAAGTT	2308
QY	266	eGlyHisIleLysLeuSerAspPheLeuThrPheAlaLeuLysSerIleValGlnLeuLe	286
Db	2309	CGGCCACCTCAAGACGTCGACTTCTTGGGCTACTCCATCAAGGCCATCACGAGGGCAT	2368
QY	286	uLeuProGluPheLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGluAs	306
Db	2369	CCTGCGGCGCGTGGCACCTACGTGGACACCAACCCCGCGCGAGTTCGACTCTCTTCCAGGA	2428
QY	306	pValLeuLysLeuTyrGluGlyIleLysLeuProGlnGlyProLeuLeuLysAlaI1	326
Db	2429	CATCATCAACCTCTATGAGGGCGGCATCAAGTGGCCAAAGGTGGCCGCCCTCGAGGAGCT	2488
QY	326	eThrAspSerIleProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLe	346
Db	2489	CCGTAGCAGTTCCTCGTCCAGCTCATCAAGGACCTCTCTCCCGTCGGCGGCGACTCCCT	2548
QY	346	uPheLysTyrProThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAspG1	366
Db	2549	GCTTAAGCTCCCCGTCACATCATCCAGGAGAACAGCAGGCGTGGAGACCGACCGA	2608
QY	366	uGluPheGlyArgGluMetLeuAlaGlyValAsnProValIleIleSerArgLeu----	384

[illegible]

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Db 3688 TGAATGTGTAAACAAATTTGGCGTCTCGCTCACTGACAGGAACGTGGTAAAAAATGC 3747
Qy 612 ArgGlyValAlaValGluAspSerSerProLeuGlyIleArgLeuLeuIleGlnAsp 631
Db 3748 AGGGGCATGCGGTGAGGACCCGTCGAGCCGTACAAGGTGCGGTGCTGGTCCGAC 3807
Qy 632 TyrProTyrAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGlu 651
Db 3808 TACCCGTACGCGCGACGGGCTGGCGATCTGGCAGCCATTGACGAGTACGTGAGCGAG 3867
Qy 652 TyrCysAsnTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAla 671
Db 3868 TACCTGGCCATCTACTACCCGAACGACGGCGTGTGACGGCGATACGGAGGTGCAGGCG 3927
Qy 672 TrpTrpLysGluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpPro 691
Db 3928 TGGTGGAAGGAGACGCGCGAGGTGCGGACGGCGACCTCAAGGACGCCCATGGTGGCC 3987
Qy 692 LysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSer 711
Db 3988 AAGATGCAAAAGTGTCCGGAGCTGGCCAAAGCGTGCACCACCATCATCTGGATCGGGTGC 4047
Qy 712 AlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArg 731
Db 4048 GCGCTGCATGGCGCAGTCAACTTCGGGGCAGTACCCCTACGCGGGGTTCCTCCCGAACCGG 4107
Qy 732 ProThrLeuSerArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLys 751
Db 4108 CCGACGGTGAGCGCGCGCGCATGCCGAGCCCGCACGGAGGTACGCGGAGCTGGAG 4167
Qy 752 ThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGly 771
Db 4168 CGCGACCCGGAGCGGGCCTTCATCCACACCATCACGAGCCAGATCCAGACCATCATCGGC 4227
Qy 772 IleSerLeuIleGluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArg 791
Db 4228 GTGTCGTGCTGGAGGTGCTGTGGAAGCACTCCTCCGACGAGCTGTACCTCGGGCAGCGG 4287
Qy 792 GluSerProGluTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLys 811
Db 4288 GACACGCGGAGTGGACCTCGGACCCCAAAGCCCTGGAGGTGTTCAAGCGGTTCAGCGAC 4347
Qy 812 LysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsn 831
Db 4348 CGGCTGGTGGAGATCGAGAGCAAGGTGGTGGGCATGAACCATGACCCCGAGCTCAAGAAC 4407
Qy 832 ArgSerGlyProValLysValProTyrThrLeuLeuPhePro---ThrSerGlu----- 848
Db 4408 CGCAACGGCCCCGGCTAAGTTTCCCTACATGCTGCTCTACCCCAACACCTCCGACCACAAG 4467
Qy 849 -----GlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862
Db 4468 GCGCGCGTGC CGGGCTTACCGCCAAGGGCATCCCCAACAGCATCTCCATC 4518
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RESULT 10
US-09-751-687-11
; Sequence 11, Application US/09751687
; Patent No. 6660915
; GENERAL INFORMATION:
; APPLICANT: Douma, Anneke
; APPLICANT: Doderer, Albert
; APPLICANT: Cameron-Mills, Verena
; APPLICANT: Skadhauge, Birgitte
; APPLICANT: Bech, Lene
; TITLE OF INVENTION: LOW LIPOXYGENASE 1 BARLEY
; FILE REFERENCE: 11225.11US01
; CURRENT APPLICATION NUMBER: US/09/751,687
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 4663
; TYPE: DNA
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; ORGANISM: Hordeum vulgare
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2346)..(2348)
; OTHER INFORMATION: "n" is a, c, t, or g encoding an acidic, basic, or polar amino ac
; OTHER INFORMATION: i
US-09-751-687-11

Alignment Scores:
Pred. No.: 7.05e-244 Length: 4663
Score: 2273.50 Matches: 503
Percent Similarity: 45.82% Conservative: 138
Best Local Similarity: 35.95% Mismatches: 212
Query Match: 50.14% Indels: 548
DB: 4 Gaps: 14

US-10-731-642A-1 (1-862) x US-09-751-687-11 (1-4663)

Qy 1 MetPheLeuGluLysIleValAspAlaIleThrGlyLysAspAspGlyLysLysValLys 20
Db 357 ATGCTGCTGGGAGGGCTGATGACACACCTCACGGGGGCGAACAAGAGCGCCGGCTCAAG 416
Qy 21 GlyThrValValLeuMetLysLysAsnValLeuAspPheThrAspIleAsnAlaSerVal 40
Db 417 GGCACGGTGGTGTCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC 476
Qy 41 LeuAspGlyValLeuGluPheLeuGlyArgArgValSerLeuGluLeuIleSerSerVal 60
Db 477 ATCGACGGCATCGGCGAGTTCCTCGCAAGGGTGTACCTGCCAGCTTATCAGCTCCACC 536
Qy 61 -----AsnAlaAspProAlaAsnGlyLeu----- 68
Db 537 GCCGTGACCAAGGTAATCACTA-CCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATA 595
Qy 68 ----- 68
Db 596 GTATTTCTTCGTGTGGCGCGGCATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 655
Qy 68 ----- 68
Db 656 AAGATAGGATAGTAGCCCTGGCGGGTCTCTTTTACCTGAGCATGGGCATATGCCATCGA 715
Qy 68 ----- 68
Db 716 AAAAAGAGACAACAGCATGCATGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 775
Qy 68 ----- 68
Db 776 CTCGAGACAAAGCAACACAACAAGAGGACGACACGTCAAAAGCAACAACAAGCAAG 835
Qy 68 ----- 68
Db 836 GACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCAC 895
Qy 68 ----- 68
Db 896 ACAATCAGCAGGCTATAAACAGTTGTTCATCAAAAAACAACGCTGGAAGAGAGAGAGGA 955
Qy 68 ----- 68
Db 956 AGGAATAGTAGCCATGAAAAATTAAATCACCGGGCGTGTCTTTGCCCAACAATTAAT 1015
Qy 68 ----- 68
Db 1016 CAAGCAGGTACGTGGCATGTATAGTTCTTTGTAAGTAAACTAAGCATGTGATATGAGAAG 1075
Qy 69 -----GlnGlyLysArgSerLysAlaAlaTyrLeuGlu 79
Db 1076 GTACGTGGTGTGCAGACAACCGCGGTGCGGGAGAGGTGGCGCGGAGCGGAGCTGGAG 1135
Qy 80 AsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPhe 99
Db 1136 CAGTGGTGACGAGCCTGCCGTGCTGACGACGCGGGGAGTCCAAGTTCGGCCTCACCTTC 1195
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Db 3329 TTCTCCACGGTCGATGTGATTCACTCACTCGATGCACAACAACTGATCGAAATATGATTG 3388

QY 525 -----LeuAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsn 539

Db 3389 ATTGAACCGCCAGGCTGAACACTCACCGGTGATGGAGCCGTTCTGATCTCGACGAAC 3448

QY 540 ArgGlnLeuSerAlaLeuHisProIleTyrLysLeuLeuHisProHisPheArgGluThr 559

Db 3449 CGGCACCTTAGCGTGACGACCCCGGTGCACAAGCTGCTAGCCCGCACTACCGCGACACC 3508

QY 560 MetAsnIleAsnAlaLeuAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGluLeu 579

Db 3509 ATGACCATCAACGCGCTGGCGCGGACGCTCATCAACCGCCGGCGCATCTTCGAGATG 3568

QY 580 ThrValPheProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpVal 599

Db 3569 ACGGTGTTCCCGGCAAGTTCGCGTTGGGATGTCGGCCGTGGTGTTACAAGGACTGGAAG 3628

QY 600 PheProGluGlnAlaLeuProThrAspLeuIleLys----- 611

Db 3629 TTCACCGAGCAGGACTGCCGACGATCTCATCAA-GAGGTACGTACCTGGTAAATGTTA 3687

QY 611 ----- 611

Db 3688 TGAATGTGTAAACAAATTTGGCGTCTCGCTCACTGACAGGAACGTGTAAAAAATGC 3747

QY 612 ArgGlyValAlaValGluAspSerSerSerProLeuGlyIleArgLeuLeuIleGlnAsp 631

Db 3748 AGGGGCATGGCGGTGGAGGACCCGTCGAGCCCGTACAAGGTGCGGTGCTGGTCCGGAC 3807

QY 632 TyrProTyrAlaValAspGlyLeuLysIleTrpSerAlaIleLysSerTrpValThrGlu 651

Db 3808 TACCCGTACGCGCGGACGGGCTGGCGATCTGGCACGCCATTTGACAGTACGTGAGCGAG 3867

QY 652 TyrCysAsnTyrTyrTyrLysSerAspAlaValGlnLysAspThrGluLeuGlnAla 671

Db 3868 TACCTGGCCATCTACTACCCGAACGACGCGCTGCTGAGGGCGATACGAGGTGCAGCG 3927

QY 672 TrpTrpLysGluLeuArgGluGluGlyHisGlyAspLysLysAspGluProTrpTrpPro 691

Db 3928 TGGTGAAGGAGACGCGCGAGGTGCGGCGACGCGACCTCAAGGACGCCCATGGTGGCCC 3987

QY 692 LysMetGlnThrValGlnGluLeuIleAspSerCysThrIleThrIleTrpIleAlaSer 711

Db 3988 AAGATGCAAAAGTGTCCGGAGCTGGCCAAAGCGTGCACCACCATCATCTGGATCGGTCG 4047

QY 712 AlaLeuHisAlaAlaValAsnPheGlyGlnTyrProTyrAlaGlyTyrLeuProAsnArg 731

Db 4048 GCGCTGCATGGCGCAGTCAACTTCGGGGAGTACCCCTACGCGGGGTCTCTCCCGAACCGG 4107

QY 732 ProThrLeuSerArgAsnPheMetProGluProGlySerProGluTyrGluGluLeuLys 751

Db 4108 CCGACGGTGAGCGCGCGCGCATGCCCGAGCCCGCACGAGGAGTACGCGGAGCTGGAG 4167

QY 752 ThrAsnProAspLysValPheLeuLysThrIleThrProGlnLeuGlnThrLeuLeuGly 771

Db 4168 CGCGACCCGAGCGGGCCCTTCATCCACACCATCACGAGCCAGATCCAGACCATCATCGGC 4227

QY 772 IleSerLeuIleGluIleLeuSerArgHisSerSerAspThrLeuTyrLeuGlyGlnArg 791

Db 4228 GTGTCGCTGCTGGAGGTGCTGTGAAAGCACTCCTCCGACGAGCTGTACCTCGGCGAGCGG 4287

QY 792 GluSerProGluTrpThrLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLys 811

Db 4288 GACACGCGGAGTGGACCTCGGACCCCAAGCCCTGGAGGTGTTCAAGCGGTTTCAGCGGAC 4347

QY 812 LysLeuSerAspIleGluAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsn 831

Db 4348 CGGCTGGTGGAGATCGAGAGCAAGGTGGTGGGCATGAACCATGACCCGGAGCTCAAGAAC 4407

QY 832 ArgSerGlyProValLysValProTyrThrLeuLeuPhePro---ThrSerGlu----- 848

Db 4408 CGCAACGGCCCGGCTAAGTTTCCCTACATGCTGTCTACCCAAACACCTCCGACCACAAG 4467

QY 849 -----GlyGlyLeuThrGlyLysGlyIleProAsnSerValSerIle 862

Db 4468 GGCGCGCTGCCGGGCTTACCGCAAGGGCATCCCCAACAGCATCTCCATC 4518

RESULT 11

US-09-714-767A-3

; Sequence 3, Application US/09714767A

; Patent No. 6709865

; GENERAL INFORMATION:

; APPLICANT: Bidney, Dennis

; APPLICANT: Duwick, Jon

; APPLICANT: Hendrick, Carol

; APPLICANT: Hu, Xu

; APPLICANT: Lu, Guihua

; APPLICANT: Crasta, Oswald

; TITLE OF INVENTION: Sunflower RHO GAP, LOX, ADH and SCIP -

; TITLE OF INVENTION: Polynucleotides and Methods of Use

; FILE REFERENCE: 35718/201902

; CURRENT APPLICATION NUMBER: US/09/714,767A

; CURRENT FILING DATE: 2000-11-16

; PRIOR APPLICATION NUMBER: US 60/166,128

; PRIOR FILING DATE: 1999-11-18

; PRIOR APPLICATION NUMBER: US 60/201,837

; PRIOR FILING DATE: 2000-05-03

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 2945

; TYPE: DNA

; ORGANISM: Helianthus annuus

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (0)...(0)

; OTHER INFORMATION: lox cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (19)....(2721)

US-09-714-767A-3

Alignment Scores:

Pred. No.: 4.82e-185 Length: 2945

Score: 1746.50 Matches: 357

Percent Similarity: 60.33% Conservative: 148

Best Local Similarity: 42.65% Mismatches: 283

Query Match: 38.52% Indels: 49

DB: 4 Gaps: 15

US-10-731-642A-1 (1-862) x US-09-714-767A-3 (1-2945)

QY 40 ValLeuAspGlyValLeuGluPheLeuGlyArgValSerLeuGluLeuSerSer 59

Db 316 ATTGTGATGGTGTCTCTGATCTCTTAGGGTTGTCATTTTGTGGAGCTCGTTTCAAAT 375

QY 60 ValAsnAlaAspProAlaAsnGlyLeuGlnGlyLysArgSerLysAlaAlaTyrLeuGlu 79

Db 376 ---GACCTCGATTCAAAAGGAACCAAAAGACAGTGAAGGCTTATGCAAGATAC--- 426

QY 80 AsnTrpLeuThrAsnSerThrProIleAlaAlaGlyGluSerAlaPheArgValThrPhe 99

Db 427 -----AACGCACCTGGATTGGACATTAGCGTGTACACATACAAATGCGACTTC 474

QY 100 AspTrpAspAspGluGluPheGlyValProGlyAlaPheIleLeuLysAsnLeuHisPhe 119

Db 475 GAC---GTCCCTGAAGATTTGGGGAGATAGGAGCTGTGTGTGTAGAAAATGAGTATAGC 531

QY 120 SerGluPhePheLeuLysSerLeuThrLeuGluAspValProAsnHisGlyLysValHis 139

Db 532 AAGAAGATGTTTTTCAAGAACATGTTCTT-----AACACGGT---GTTACC 576

QY 140 PheValCysAsnSerTrpValTyrProAlaAsnLysTyrLysSerAspArgIlePhePhe 159









QY	565	uAlaArgGlnIleLeuIleAsnGlyGlyGlyLeuLeuGlu-----LeuThrValPh	582
Db	1224	CGCACGCAAGGCCTGCTCGACGCGCGGGTGTTTCGACGACTTCATCGCGACAGGCGG	1283
QY	582	eProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTirValPheProG1	602
Db	1284	CCCCGACAAGGCGCACCTCCAGTTGGGCAAGAAGGGCTTCAGCGCTGGACGCTGGCGGA	1343
QY	602	uGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerSerPr	622
Db	1344	CAACAAGCCCCGTGTGACCTGGAGCGCGGGCGTGCTG-----GACCC	1388
QY	622	oLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTr	642
Db	1389	T-----GCCGTGCTCCCAACTACCCGTACCGGGACGACGCCCTGCCCTTGTG	1436
QY	642	pSerAlaIleLysSerTirpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAl	662
Db	1437	GGACGCGTTCGAGAGTACGTGGCGCGCTCCTCAGGCACTTCTACCGACCGATGCCGA	1496
QY	662	aValGlnLysAspThrGluLeuGlnAlaTirpTyrLysGluLeuArgGluGlyHisG1	682
Db	1497	CCTCGAGGCGGACACCGAGATGCAGCAATGTTGGAAGGACCTCACCGAG-----CACGG	1550
QY	682	yAspLysLysAspGluProTirpTirpProLysMetGlnThrValGlnGluLeuIleAspSe	702
Db	1551	GCTGCCCGTGGACAAGTCCCTGCCGGAGCTGGCGCGCTCGACGACCTGGTCGACAT	1610
QY	702	rCysThrIleThrIleTirpIleAlaSerAlaLeuHisAlaAlaValAsnPheGlyGlnTy	722
Db	1611	CCTCACCACCGTCTTTCACGGTCAGCGTGCAGCACGCGCGGTGAACCTACCTGCAATA	1670
QY	722	rProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetPro---G1	741
Db	1671	CGACCACTACGCCCTTCGTACCGAATGCCCCCTGAGCATGCGCGGGAGCCACCCGCCA	1730
QY	741	uProGlySerProGluTyrGluGluLeuLysThrAsnProAspLysValPheLeuLysTh	761
Db	1731	GAAGGGACGCTGCTGCAGAGGACATC-----CCCGAGATGATTCCACCAAGTC	1781
QY	761	rIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHi	781
Db	1782	C-----CAGATGCTCTGGCAGGTGCGCATCGGCGCGCTCTCCAGCTT	1826
QY	781	sSerSerAspThrLeuTyrLeu-----GlyGlnArgGluSerProGluTirpTh	797
Db	1827	CGGAGACGACGAGGAGTACCTGTGCACGAGGCGGCTGGCGCGAG-----GAGTACTT	1880
QY	797	rLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleG1	817
Db	1881	CCACGAACCGGAGCTGGTGGCCATCCGCCAGCGGTTCCAGGAGCGCTGCGGCCCGAGCG	1940
QY	817	uAspGlnIleMetGlnMetAsnValAspGluLysTirpLysAsnArgSerGlyProVally	837
Db	1941	CGAGCGCGTG-----GAGCGCGCAACGCGGCGCGCGGA	1973
QY	837	sValProTyrThrLeuLeuPhePro	845
Db	1974	GGTGCCTACACCATCCTGCGTCCC	1998

## RESULT 15

RES011 13  
 US-09-540-540-1264  
 ; Sequence 1264, Application US/09902540  
 ; Patent No. 6833447  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Wiegand, Roger C.  
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
 ; FILE REFERENCE: 38-10(15849)B  
 ; CURRENT APPLICATION NUMBER: US/09/902,540

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; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1264
; LENGTH: 41310
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(41310)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1264

Alignment Scores:
Pred. No.:          9.15e-50          Length:          41310
Score:             559.50             Matches:         175
Percent Similarity: 43.80%             Conservative:    118
Best Local Similarity: 26.16%           Mismatches:      236
Query Match:       12.34%             Indels:          140
DB:                4                  Gaps:            23

US-10-731-642A-1 (1-862) x US-09-902-540-1264 (1-41310)
QY      219 ProValLeuGlyGlySerSerGluTyrProTyrProArgArgGly-----ArgThr 235
Db      38481 CCCTTCTACCGGTGGTGGTGGTGGCGCCACCGTCCGAGTGTCTCGAGGGACCGCGAA 38540
QY      236 GlyArgLysProThrLys-ThrAspProAsnSerGluSerArgIleProLeuLeuMet-- 254
Db      38541 GCTCGTCCGACGAGCAAGCAGCGAGCGGAGTCCACGGCGCGCGAGCTGCTCGAGGC 38600
QY      255 -----SerLe 256
Db      38601 CCGCCAGCGGATGTACCCGTGGCGCGCGCTGAGATGACCGAGGGCTTCCCGCGCGCT 38660
QY      256 uAspIleTyr-----ValProArgAspGluArgPheGlyHisIleLysLeuSe 272
Db      38661 CGACCTCCGTGAGGGAGGCGCGTCCGAAGGACGAGTCTACCGGGCGCTGACGGAGGG 38720
QY      272 rAspPheLeuThrPheAlaLeuLysSerIle-----ValGlnLeuLeuProGluPh 290
Db      38721 CAGCTACGAAGTGGTTCATCGCGAAGACGCTGGCGGCCATCAAGCTGAACCTGCCCATGCT 38780
QY      290 eLysAlaLeuPheAspSerThrHisAsnGluPheAspSerPheGluAspValLeuLysLe 310
Db      38781 GACCCGCGCCTGGAACGGGCTGGTGGACATCTTCGACTTCTTCAAACAC----- 38820
QY      310 uTyrGluGlyGlyIleLysLeuProGlnGlyProLeuLeuLysAlaIleThrAspSerIl 330
Db      38829 ----- 38829
QY      330 eProLeuGluIleLeuLysGluLeuLeuArgSerAspGlyGluGlyLeuPheLysTyrPr 350
Db      38830 ----CTGGAGGTG----- 38838
QY      350 oThrProGlnValIleGlnGluAspLysThrAlaTrpArgThrAspGluGluPheGlyAr 370
Db      38839 ----CCCCAGCTCGCCACGCGC-----TGGAAGGACGACCTCGAGTTCGCGCG 38882
QY      370 gGluMetLeuAlaGlyValAsnProValIleIleSerArgLeuGlnGluPheProProLy 390
Db      38883 GCAGGCGCTCCAGGGCATCGCCCCCTCCACATCACGCTCGTCCCCAGTCTGCCG----- 38937
QY      390 sSerLysLeuAspProLysIleTyrGlyAsnGlnAsnSerThrIleThrArgGluGlnIl 410
Db      38938 -----CAGGGCATGCGCGTCCACCGACGACGACGCT 38966
QY      410 eGluAspLysLeuAsp---GlyLeuThrIleAspGluAlaIleLysThrAsnArgLeuPh 429
Db      38967 CCGGGGCTCTTGTGCGCCCGGACACGCTGGCCAGGGGCGCTCGACGCCAAGCGCATCTT 39026
QY      429 eIleLeuAsnHisHis-----AspIleLeuMetProTyrLeuArgArgIleAsnThrSe 447

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Db 39027 CCTGATCGACTTCGAAATCCTCGACGACATCAGGATGTACCGAAGGTCCGCGAGGACGG 39086  
QY 447 rThrAspThrLysThrTyr-----AlaSerArgThrLeuLeuPheLeuGlnAspAsnG1 465  
Db 39087 AGTCGAGGAGCGGCGCTGGCTCCCGCGGCGGCTGCCTGTGTACCTGGATGACACGCG 39146  
QY 465 yThrLeuLysProSerAlaIleGluLeuSerLeuProHisProAspGlyAspGlnPheG1 485  
Db 39147 TCAACTCGACCCCTGGCCATCCAGCTCGGG-----CGGGACGC 39185  
QY 485 yAlaValSerLysValTyrThrProAlaAspGlnGlyValGluGlySerIleTrpGlnLe 505  
Db 39186 CCAGAAGGACCCTGTCTTCACGCCGAACGACGACGCGTACGAC-----TGGCTCGC 39236  
QY 505 uAlaLysAlaIleAlaAlaValAsnAspSerGlyValHisGlnLeuIleSerHisTrpLe 525  
Db 39237 CGCGAAATCTACCTCCGGTGCAGCGAGGCAACTCGCACCATGATGGTGTGCGACGGCT 39296  
QY 525 uAsnThrHisAlaAlaIleGluProPheValIleAlaThrAsnArgGlnLeuSerAlaLe 545  
Db 39297 GCGCACACACTTCGTGGCGGAGCCGTTCTGTCATGGCGACGATGCGCAACCTGCCGGACCC 39356  
QY 545 uHisProIleTyrLysLeuLeuHisProHisPheArgGluThrMetAsnIleAsnAlaLe 565  
Db 39357 GCACCCCGTCTACAAACTGCTGGCGGCGCACTTCGGTACACGCTCGCCATCAACGAGGG 39416  
QY 565 uAlaArgGlnIleLeuIleAsnGlyGlyLeuLeuGlu-----LeuThrValPh 582  
Db 39417 CGCACGCAAGGCCCTGCTCGACGCGAGCGGGGTGTTTCGACGACTTCATCGCGACAGCGG 39476  
QY 582 eProAlaLysTyrSerMetGluMetSerAlaValValTyrLysAspTrpValPheProG1 602  
Db 39477 CCCCACAAAGGCCACCTCCAGTTGGGCAAGAAGGGCTTCCAGCGCTGGACGCTGGCGGA 39536  
QY 602 uGlnAlaLeuProThrAspLeuIleLysArgGlyValAlaValGluAspSerSerPr 622  
Db 39537 CAACAAGCCCCGTGTGACCTGGAGCGGCGGGCGGTGTG-----GACCC 39581  
QY 622 oLeuGlyIleArgLeuLeuIleGlnAspTyrProTyrAlaValAspGlyLeuLysIleTr 642  
Db 39582 T-----GCCGTGCTCCCACTACCCGTACCGGACGACGCCCTGCCCTTGTG 39629  
QY 642 pSerAlaIleLysSerTrpValThrGluTyrCysAsnTyrTyrTyrLysSerAspAl 662  
Db 39630 GGACGCGTTTCGAGGAGTACGTGGCGGCGTCTCAGGCACCTTCTACCGACCCGATGCCGA 39689  
QY 662 aValGlnLysAspThrGluLeuGlnAlaTrpTrpLysGluLeuArgGluGluGlyHisG1 682  
Db 39690 CCTCGAGGCCGACACCGAGATGCAGCAATGGTGAAGGACCTCACCGAG-----CACGG 39743  
QY 682 yAspLysLysAspGluProTrpTrpProLysMetGlnThrValGlnGluLeuIleAspSe 702  
Db 39744 GCTGCCCCGTGGACAAGCTGCCCTGCCGGGAGCTGCCCGCGTTCGACGACCTGGTCGACAT 39803  
QY 702 rCysThrIleThrIleTrpIleAlaSerAlaLeuHisAlaValAsnPheGlyGlnTy 722  
Db 39804 CCTCACCCACCGTCTCTTCACGGTTCAGCGTGCAGCACGCGGGGTGAACCTACCTGCAATA 39863  
QY 722 rProTyrAlaGlyTyrLeuProAsnArgProThrLeuSerArgAsnPheMetPro--G1 741  
Db 39864 CGAGCACTACGCTTCGTACCGAATGCGCCCTGAGCATGCGCGGAGCCACCCCGCCA 39923  
QY 741 uProGlySerProGluTyrGluGluLysThrAsnProAspLysValPheLeuLysTh 761  
Db 39924 GAAGGGACGTCGTCGTCAGAGGACATC-----CCCGAGATGATTCACCAAGTC 39974  
QY 761 rIleThrProGlnLeuGlnThrLeuLeuGlyIleSerLeuIleGluIleLeuSerArgHi 781  
Db 39975 C-----CAGATGCTCTGGCAGGTTCGCCATCGGCCCGGCGCTCTCCAGCTT 40019  
QY 781 sSerSerAspThrLeuTyrLeu-----GlyGlnArgGluSerProGluTrpTh 797

Db 40020 CGGAGACGACGAGGAGTACCTGTGTGCACGAGGGCGGTGGCGCGAG-----GAGTACTT 40073  
QY 797 rLysAspGlnGluProLeuSerAlaPheAlaArgPheGlyLysLysLeuSerAspIleG1 817  
Db 40074 CCACGAACCGGAGCTGGTGGCCATCCCGCAGCGGTTCCAGGAGCGCTGCGCGCCAGCG 40133  
QY 817 uAspGlnIleMetGlnMetAsnValAspGluLysTrpLysAsnArgSerGlyProValLy 837  
Db 40134 CGAGGCGGTG-----GAGGCGCGCAACGCGGCGCGCGA 40166  
QY 837 sValProTyrThrLeuLeuPhePro 845  
Db 40167 GGTGCCCTACACCATCCTGCGTCCC 40191

Search completed: March 14, 2005, 10:34:42  
Job time : 489 secs



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